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                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:           February 28, 2004, 03:39:37 ; Search time 4277 Seconds
                                            (without alignments)
                                            12595.598 Million cell updates/sec


Title:            US-09-668-314C-1
Perfect score:    1804
Sequence:         1 atgggcgcactggcccgggc..........aaaccaaaaaaaaaaaaaaa 1804


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:        55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        EST:*
                  1:   em_estba:*
                  2:   em_esthum:*
                  3:   em_estin:*
                  4:   em_estmu:*
                  5:   em_estov:*
                  6:   em_estpl:*
                  7:   em_estro:*
                  8:   em_htc:*
                  9:   gb_est1:*
                  10:  gb_est2:*
                  11:  gb_htc:*
                  12:  gb_est3:*
                  13:  gb_est4:*
                  14:  gb_est5:*
                  15:  em_estfun:*
                  16:  em_estom:*
                  17:  em_gss_hum:*
                  18:  em_gss_inv:*
                  19:  em_gss_pln:*
                  20:  em_gss_vrt:*
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     28:   gb_gss1:*
     29:   gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1182.2	65.5	3703	11	AK078770	AK078770 Mus muscu
	2	1177.8	65.3	1810	11	AK052309	AK052309 Mus muscu
	3	1114.4	61.8	1245	29	AY419487	AY419487 Homo sapi
c	4	910	50.4	970	13	BQ688240	BQ688240 AGENCOURT
c	5	894.4	49.6	1015	13	BX401345	BX401345 BX401345
	6	855.8	47.4	1245	29	AY419489	AY419489 Mus muscu
	7	821.6	45.5	1004	13	BX401346	BX401346 BX401346
	8	815.8	45.2	970	29	AY419488	AY419488 Pan trogl
	9	815.2	45.2	908	13	BU179147	BU179147 AGENCOURT
	10	800.6	44.4	912	14	CA489608	CA489608 AGENCOURT
	11	798.8	44.3	968	13	BQ945383	BQ945383 AGENCOURT
	12	792.4	43.9	890	14	CA454208	CA454208 AGENCOURT
	13	785.2	43.5	902	14	CA488936	CA488936 AGENCOURT
	14	777.4	43.1	836	14	CA487940	CA487940 AGENCOURT
	15	777.4	43.1	843	12	BG281374	BG281374 602401870
	16	762.6	42.3	963	13	BQ935923	BQ935923 AGENCOURT
	17	759.8	42.1	925	13	BX390813	BX390813 BX390813
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	23	727	40.3	887	13	BQ881371	BQ881371 AGENCOURT
	24	725.8	40.2	940	14	CF408400	CF408400 CH3#054_C
c	25	723.4	40.1	730	14	CA448122	CA448122 UI-H-ED1-
	26	717.6	39.8	814	12	BG106472	BG106472 602289863
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	28	713	39.5	713	12	BM772694	BM772694 K-EST0056
	29	709.6	39.3	854	12	BG533371	BG533371 601860758
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RESULT 1
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LOCUS   AK078770   3703 bp   mRNA   linear   HTC 18-SEP-2003
DEFINITION   Mus musculus 15 days embryo male testis cDNA, RIKEN full-length
               enriched library, clone:8030470O09 product:beta-site APP-cleaving
               enzyme 2, full insert sequence.
ACCESSION   AK078770
VERSION   AK078770.1 GI:26347470
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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               Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
               Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
               sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
               FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3703)

AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
     source   1. .3703
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                     /mol_type="mRNA"
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                     /db_xref="GI:26347471"
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                     IPKGFNSSFLVNIATIFESENFFLPGIKWNGILGLAYAALAKPSSSLETFFDSLVAQA
                     KIPDIFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILK
                     LEIGGQNLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVVEAVARTSLIPEFSDGFWT
                     GAQLACWTNSETPWAYFPKISIYLRDENASRSFRITILPQLYIQPMMGAGFNYECYRF
                     GISSSTNALVIGATVMEGFYVVFDRAQRRVGFAVSPCAEIEGTTVSEISGPFSTEDIA

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                    SNCVPAQALNEPILWIVSYALMSVCGAILLVLILLLLLPLHCRHAPRDPEVVNDESSL
                    VRHRWK"
ORIGIN

   Query Match              65.5%;   Score 1182.2;   DB 11;   Length 3703;
   Best Local Similarity    80.6%;   Pred. No. 1.6e-164;
   Matches 1447;  Conservative    0;  Mismatches  308;  Indels   40;  Gaps     4;


Qy       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
           | ||| | |||||||||||||||||||||||||||||||||||| ||||||| ||||||||||
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Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
           | |  || || |    || ||||  ||| || ||||||||| |   || || ||||| || ||
Db     162 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCCGGGTTGCCCCGGGCCGATGGTCTG 221


Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
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Qy      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Db      870  TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  929

Qy      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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RESULT 2
AK052309
LOCUS        AK052309                1810 bp    mRNA    linear    HTC 20-SEP-2003
DEFINITION   Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
             library, clone:D330025D14 product:beta-site APP-cleaving enzyme 2,
             full insert sequence.
ACCESSION    AK052309
VERSION      AK052309.1  GI:26342548
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
  AUTHORS    Carninci,P. and Hayashizaki,Y.
  TITLE      High-efficiency full-length cDNA cloning
  JOURNAL    Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE    99279253
   PUBMED    10349636
REFERENCE    2
  AUTHORS    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL    Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE    20499374
   PUBMED    11042159
REFERENCE    3
  AUTHORS    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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  TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
  JOURNAL    Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE    20530913
   PUBMED    11076861
REFERENCE    4
  AUTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
```

FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 1810)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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Db   62 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCCGGTGCTGGCGCAGTGGCTCTTGAGTGCG 121

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Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Qy   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy     841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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RESULT 3
AY419487
LOCUS       AY419487                1245 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY419487
VERSION     AY419487.1  GI:39775444
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 1245)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1245)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
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COMMENT         These sequences were made by sequencing genomic exons and ordering
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Matches 1115;  Conservative   0;  Mismatches 130;  Indels   0;  Gaps   0;


Qy      313 CTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCC 372
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Qy      433 GTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACC 492
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Qy      793 TATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA 852
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Qy      1033 TGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGAT 1092
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Qy      1093 GAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATG 1152
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Qy      1153 ATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCG 1212
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Qy      1213 CTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAG 1272
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Qy      1333 TCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGC 1392
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Db      1021 TCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGC 1080

Qy      1393 GAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTT 1452
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RESULT 4
BQ688240/c
LOCUS   BQ688240   970 bp   mRNA   linear   EST 15-JUL-2002
DEFINITION AGENCOURT_8034236 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208269
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ACCESSION   BQ688240
VERSION   BQ688240.1 GI:21813556
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 970)

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                        /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                        Site_2: EcoRI; cDNA made by oligo-dT priming.
                        Directionally cloned into EcoRI/XhoI sites using the
                        following 5' adaptor: GGCACGAG(G). Library constructed by
                        Ling Hong in the laboratory of Gerald M. Rubin (University
                        of California, Berkeley) using ZAP-cDNA synthesis kit
                        (Stratagene) and Superscript II RT (Life Technologies).
                        Note: this is a NIH_MGC Library."
ORIGIN

  Query Match   50.4%; Score 910; DB 13; Length 970;
  Best Local Similarity   98.3%; Pred. No. 2.5e-124;
  Matches 930; Conservative   0; Mismatches   15; Indels   1; Gaps   1;

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             |||||||||||||||||||| |||||| |||||||||||||||||||||||||||||||||
Db   954 GAAATTCTGAAATTGGAATTTGGAGCCCAAAGCCTTAATCTGGACTGCAGAGAGTATAAC 895

Qy   889 GCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTT 948
             |||| |||||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db   894 GCAGCCAAGGCCATCGTGACCAGTGGCACCCCGCTGCTGCGCCTGCCCCAGAAGGTGTTT 835

Qy   949 GATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTC 1008
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   834 GATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGTTTTC 775

Qy   1009 TGGACTGGGTCCC-AGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC 1067
             ||||||||||||| |||||||||||||||||||||||||||||||||||||||| | |||
Db   774 TGGACTGGGTCCCAAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTACTTCCCC 715

Qy   1068 TAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 1127
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   714 TAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 655

```
Qy    1128 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATT 1187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     654 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATT 595

Qy    1188 CGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTA 1247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 CGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTA 535

Qy    1248 CGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAAT 1307
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 CGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAAT 475

Qy    1308 TGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTAACAGAGGATGTAGCCAGCAA 1367
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 TGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTAACAGAGGATGTAGCCAGCAA 415

Qy    1368 CTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCAT 1427
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 CTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCAT 355

Qy    1428 GAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTG 1487
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 GAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTG 295

Qy    1488 TCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCG 1547
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 TCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCG 235

Qy    1548 CTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATC 1607
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 CTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATC 175

Qy    1608 ACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTT 1667
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     174 ACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTT 115

Qy    1668 CAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTC 1727
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     114 CAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTC 55

Qy    1728 AAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAAAAAAAA 1773
           ||||||||||||||||||||||||||||||||||| ||   ||||||||
Db      54 AAGCTTTCAAATCCTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAA 9
```

RESULT 5
BX401345/c
LOCUS   BX401345   1015 bp   mRNA   linear   EST 13-MAY-2003
DEFINITION BX401345 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK012YC20 3-PRIME, mRNA sequence.
ACCESSION   BX401345
VERSION   BX401345.1 GI:30614534
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 1015)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
  COMMENT   Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 10331.f For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CSODK012BB10NP1&cluster=10331.f. Contact :
             Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CSODK012BB10NP1.
FEATURES   Location/Qualifiers
     source   1. .1015
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODK012YC20"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match   49.6%;   Score 894.4;   DB 13;   Length 1015;
  Best Local Similarity   97.5%;   Pred. No. 4.9e-122;
  Matches 948; Conservative   12; Mismatches   6; Indels   6; Gaps   5;

Qy   827 TAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATA 886
            |||||||||||||| |||||||||||||||:||||||||||||||||||||||||||||||
Db   1015 TAGAAATTCTGAAA-TGGAAATTGGAGGCMAAAGCCTTAATCTGGACTGCAGAGAGTATA 957

Qy   887 ACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGT 946
            ||||||||||||||||||||||||||||||||||||||||: |||||||||||||||||
Db   956 ACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTS--GCGCCTGCCCCAGAAGGTGT 899

Qy   947 TTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTT 1006
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   898 TTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTT 839

Qy   1007 TCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCC 1066
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838 TCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCC 779

Qy   1067 CTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCC 1126
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   778 CTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCC 719

Qy   1127 TGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGAT 1186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db       718 TGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGAT 659

Qy      1187 TCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCT 1246
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       658 TCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCT 599

Qy      1247 ACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAA 1306
             ||||||||||||||||||||||||||||||| ||:|||||||||||||||||||||||||
Db       598 ACGTCATCTTCGACAGAGCCCAGAAGAGGGT-GGSTTCGCAGCGAGCCCCTGTGCAGAAA 540

Qy      1307 TTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCA 1366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       539 TTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCA 480

Qy      1367 ACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCA 1426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       479 ACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCA 420

Qy      1427 TGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGT 1486
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       419 TGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTG-CGTTCCGGT 361

Qy      1487 GTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATC 1546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       360 GTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATC 301

Qy      1547 GCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAAT 1606
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db       300 GCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAAW 241

Qy      1607 CACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCT 1666
             |||||||||||||||||||||:|||||||||:|||||||||:|||||||||||||||:||:
Db       240 CACATTTCCAGGGCAGCAGCMGGGATCGAHGGTGGCGCTHTCTCCTGTGCCCACCCSTCH 181

Qy      1667 TCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTT 1726
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       180 TCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATACACTGTCTTTTGATTCTTGATTTT 121

Qy      1727 CAA-GCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTA 1785
             ||| |||||||||||||||| :|||||||||:||||||||||||||||||||||||||||
Db       120 CAAGGCTTTCAAATCCTCCCGRCTTCCAAGAMAAATAATTAAAAAAAAAACTTCATTCTA 61

Qy      1786 AACCAAAAAAAA 1797
             | :|||||| | |
Db        60 ATYCAAAACAGA 49
```

RESULT 6
AY419489
LOCUS   AY419489   1245 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Mus musculus BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY419489
VERSION   AY419489.1 GI:39775446
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus

  Query Match   47.4%; Score 855.8; DB 29; Length 1245;
  Best Local Similarity   76.6%; Pred. No. 2.2e-116;
  Matches 953; Conservative   0; Mismatches 291; Indels   0; Gaps   0;

Qy   314 TACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCT 373
            |||||||||| || ||||||||||||||||||||| || |||||||| |||| |||||||
Db   2 TACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGTGCCCCACACTCCT 61

Qy   374 ACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACG 433
            |||||||||| |||||||||| ||||||| || |||||||||| ||||||||||||||| |
Db   62 ACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCCAAGGGCTTTGATG 121

Qy   434 TCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCA 493
            |||| |||||||||||||||| ||||||||||| ||||| ||||| || |||||| |||||||
Db   122 TCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAGGACCTTGTCACCA 181

Qy   494 TCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTGAATCAGAGA 553
            |||| ||||||||||| | ||||| | ||||| ||||||||||||||| || || ||||
Db   182 TCCCAAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATTTTCGAGTCTGAGA 241

Qy   554 ATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTG 613
            |||||||||||||||| ||||||||||||||||||| |||||| || ||||||||| | | |
Db   242 ATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCTTATGCTGCTTTGG 301

Qy   614 CCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCC 673
            |||||

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Db    302  CCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  361

Qy    674  CCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCA  733

Db    362  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  421

Qy    734  ACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGT  793
                       ||| |||||||| ||||||||||||||||||||||||||||| |||||||
Db    422  NNNNNNNNNNNNNNNNGTCCTGGGTGGGATTGAACCAAGTTTGTATAAAGGAGATATCTGGT  481

Qy    794  ATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAG  853
           ||||||| ||||| || || ||||||||| || ||||||| ||||| |||||||||||||
Db    482  ATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAGTTGGAAATTGGAG  541

Qy    854  GCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTG  913
           |||| | ||| || |||||||||||||||||||||||||||||||||| |||||||||||
Db    542  GCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATTGTGGACAGTG  601

Qy    914  GCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCC  973
           ||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||| |
Db    602  GCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTGGAAGCTGTGGCAC  661

Qy    974  GCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCT  1033
           |  |||||||||||||| || |||||||| ||||||| ||| ||||||||||| ||||
Db    662  GAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCCCAGCTGGCATGCT  721

Qy    1034 GGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATG  1093
           |||| ||||| ||||| || ||| | || ||||||||| || || ||||||||||||||||
Db    722  GGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATCTACCTGAGAGATG  781

Qy    1094 AGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGA  1153
           |||| |||| | || |||||| ||||| || || || ||||| ||||||||||||||||||
Db    782  AGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCCACAGCTCTACATTCAGCCCATGA  841

Qy    1154 TGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGC  1213
           |||| || || | |||||||||||| |||||| || || || || ||| | |||||||||||
Db    842  TGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCTTCCACAAATGCGC  901

Qy    1214 TGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGA  1273
           ||||||| ||||| || ||||||||| |||||||||||| |||| ||||||||| |||| ||
Db    902  TGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGACAGAGCTCAGAGGA  961

Qy    1274 GGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  1333
           ||||||||| |||| ||| ||||||||||| |||| ||| | |||||||||||||||||||
Db    962  GGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACAGTGTCTGAAATTT  1021

Qy    1334 CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCG  1393
           | ||||| || || || || || || ||||||||||||||||| || || ||| || ||| |
Db    1022 CTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCACAGGCTCTGAATG  1081

Qy    1394 AGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTG  1453
           ||||||| ||||||||||||||||||||| || || |||||| || ||||||||||| | |
Db    1082 AGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGAGCCATTCTCCTGG  1141

Qy    1454 TCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGG  1513
           | | ||| |||| ||||||||||| ||| | || || | | ||||||| ||||||||||
Db    1142 TTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCCCGAGACCCTGAGG  1201
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Qy      1514 TCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
             |  ||  ||  ||||||||||| ||  ||||||||||||||||||||||
Db      1202 TAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1245
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RESULT 7
BX401346

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LOCUS       BX401346              1004 bp    mRNA    linear    EST 13-MAY-2003
DEFINITION  BX401346 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK012YC20 5-PRIME, mRNA sequence.
ACCESSION   BX401346
VERSION     BX401346.1  GI:30618464
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1004)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 10331.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK012BB10QP1&cluster=10331.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK012BB10QP1.
FEATURES             Location/Qualifiers
     source          1. .1004
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK012YC20"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

```
  Query Match              45.5%;  Score 821.6;  DB 13;  Length 1004;
  Best Local Similarity    99.9%;  Pred. No. 2.5e-111;
  Matches  821;  Conservative   1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       180 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 239
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Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
           ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db     240 GCCCCGGAGCTGGCMCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 299

Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 359

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 419

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 479

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 539

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 599

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 659

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 719

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 779

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 839

Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 899

Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 959

Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTAC 822
           ||||||||||||||||||||||||||||||||||||||||||
Db     960 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTAC 1001
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RESULT 8
AY419488
LOCUS   AY419488   970 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Pan troglodytes BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence,

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                 genomic survey sequence.
ACCESSION        AY419488
VERSION          AY419488.1  GI:39775445
KEYWORDS         GSS.
SOURCE           Pan troglodytes (chimpanzee)
  ORGANISM       Pan troglodytes
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE        1  (bases 1 to 970)
  AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                 Adams,M.D. and Cargill,M.
  TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
                 gene trios
  JOURNAL        Science 302 (5652), 1960-1963 (2003)
   PUBMED        14671302
REFERENCE        2  (bases 1 to 970)
  AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                 Adams,M.D. and Cargill,M.
  TITLE          Direct Submission
  JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                 Rockville, MD 20850, USA
  COMMENT        These sequences were made by sequencing genomic exons and ordering
                 them based on alignment.
FEATURES                 Location/Qualifiers
     source              1. .970
                         /organism="Pan troglodytes"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:9598"
     gene                <1. .>970
                         /gene="BACE2"
                         /locus_tag="HCM6907"
ORIGIN

   Query Match              45.2%;  Score 815.8;  DB 29;  Length 970;
   Best Local Similarity    84.5%;  Pred. No. 1.8e-110;
   Matches  820;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;


Qy       334 GGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGAC 393
             |||||||||||||||  |||||||||||||||           ||||||||||||||  |
Db         1 GGAAGCAGTAACTTTGNNNTGGCAGGAACCCCGCNNNNNNNNNATAGACACGTACTTNNNC 60


Qy       394 ACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAA 453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAA 120


Qy       454 GGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACT 513
             |||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||||
Db       121 GGAAGCTGGACGGGTTTCGTTGGGGAAGACTTCGTCACCATCCCCAAAGGCTTCAATACT 180


Qy       514 TCTTTTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATT 573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TCTTTTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATT 240
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Qy      574 AAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTG 633
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGNNNNNNNNNNNNNNN 300

Qy      634 GAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAG 693

Db      301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy      694 ATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTG 753
                                                                    ||||||
Db      361 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCTTG 420

Qy      754 GGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAG 813
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAG 480

Qy      814 TGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGAC 873
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGAC 540

Qy      874 TGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTG 933
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      541 TGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGTCTG 600

Qy      934 CCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAA 993
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      601 CCCCAGAAGGTGTTTGATGCAGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAA 660

Qy      994 TTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCT 1053
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCT 720

Qy     1054 TGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTC 1113
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      721 TGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTC 780

Qy     1114 CGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTAT 1173
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTAT 840

Qy     1174 GAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTG 1233
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      841 GAATGTTACCGATTCGGCATTTCCCCATCCACAAACGCGCTGGTGATCGGTGCCACGGTG 900

Qy     1234 ATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC 1293
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGAGGGCTTCTATGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC 960

Qy     1294 CCCTGTGCAG 1303
            ||||||||||
Db      961 CCCTGTGCAG 970
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RESULT 9
BU179147
LOCUS   BU179147   908 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION AGENCOURT_8050401 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089176

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                5', mRNA sequence.
ACCESSION       BU179147
VERSION         BU179147.1  GI:22693131
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 908)
  AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
  TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL       Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: DCTD/DTP
                 cDNA Library Preparation: Rubin Laboratory
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Agencourt Bioscience Corporation
                 Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM2328  row: i  column: 17
                High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6089176"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

     Query Match              45.2%;  Score 815.2;  DB 13;  Length 908;
     Best Local Similarity    97.9%;  Pred. No. 2.3e-110;
     Matches  879;  Conservative    0;  Mismatches   13;  Indels    6;  Gaps     5;


Qy       424 GGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGAC 483
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGAC 60


Qy       484 CTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 543
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 120


Qy       544 GAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTAT 603
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTAT 180
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Qy     604 GCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA 663
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA 240

Qy     664 GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGA 723
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGA 300

Qy     724 TCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGA 783
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGA 360

Qy     784 GACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTG 843
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTG 420

Qy     844 GAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATC 903
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATC 480

Qy     904 GTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAA 963
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAA 540

Qy     964 GCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG 1023
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG 600

Qy    1024 CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTAC 1083
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTAC 660

Qy    1084 CTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATT 1143
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATT 720

Qy    1144 CAGCCCATGATGGGGGCCGG-CCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATC 1202
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     721 CAGCCCATGATGGGGGCCGGCCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATC 780

Qy    1203 CACAAATGC-GCTGGTGATCGGTGCCACGGT--GATGGAGGGCTTCTACGTCATCTTCGA 1259
           ||||||||| |||||||||||||||||||||      |  ||  |||||||||||||||| |
Db     781 CACAAATGCGGCTGGTGATCGGTGCCACGGTTGATGGAGGGCCTTCTACGTCATCTTCCA 840

Qy    1260 CAGAGCCCAGAAGAGGGT-GGGCTTCGCAGCGAG-CCCCTGTGCAGAAATTGCAGGTG 1315
           |||| |||| ||||||||| ||| ||| ||||||| |||||||||| |||||||||| |
Db     841 CAGACCCCAAAAGAGGGTGGGGTTTCCCAGCGAGCCCCCTGTGCAAAAATTGCAGGGG 898


RESULT 10
CA489608
LOCUS       CA489608                    912 bp    mRNA    linear    EST 14-NOV-2002
DEFINITION  AGENCOURT_10810689 MAPcL Homo sapiens cDNA clone IMAGE:6722086 5',
            mRNA sequence.
ACCESSION   CA489608
VERSION     CA489608.1  GI:24952399
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KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 912)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Kristi A. Egland, Ira Pastan
              cDNA Library Preparation: Invitrogen Corp
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM14284  row: d  column: 22
             High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6722086"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

   Query Match              44.4%;  Score 800.6;  DB 14;  Length 912;
   Best Local Similarity    97.5%;  Pred. No. 3.2e-108;
   Matches  857;  Conservative     0;  Mismatches   14;  Indels    8;  Gaps    4;


Qy       440 TGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCA 499
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCA 60


Qy       500 AAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCT 559
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCT 120


Qy       560 TTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGC 619
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGC 180


Qy       620 CATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACG 679
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  CATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACG 240

Qy      680  TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 739
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 300

Qy      740  GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 799
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 360

Qy      800  CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 859
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 420

Qy      860  GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 919
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 480

Qy      920  CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCAT 979
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCAT 540

Qy      980  CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 1039
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 600

Qy      1040 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 1099
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  .
Db      601  ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 660

Qy      1100 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGG 1159
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGG 720

Qy      1160 CCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCAC-AAATGCGCTGGTG 1218
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      721  CCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAAATGCGCTGGTG 780

Qy      1219 ATCGGTGC---CACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGA---AG 1272
             ||||||||   |     |     |||||||||||||||||||||||||||||||||   |
Db      781  ATCGGTGCCCACGGTGAATGGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAAAAGAA 840

Qy      1273 AGGGTGGGCTTCGCAGCG-AGCCCCTGTGCAGAAATTGC 1310
             ||  ||||||||||||| | |||||||||||||| |||
Db      841  GGGTGGGGCTTCGCAGCGAACCCCCTGTGCAGAAAATGC 879


RESULT 11
BQ945383
LOCUS        BQ945383                968 bp    mRNA     linear    EST 21-AUG-2002
DEFINITION   AGENCOURT_10030827 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6481468
             5', mRNA sequence.
ACCESSION    BQ945383
VERSION      BQ945383.1  GI:22360861
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
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ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 968)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2662  row: o  column: 05
           High quality sequence start: 26
           High quality sequence stop: 689.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6481468"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
```

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Query Match              44.3%;  Score 798.8;  DB 13;  Length 968;
Best Local Similarity    97.6%;  Pred. No. 5.7e-108;
Matches  853;  Conservative    0;  Mismatches   17;  Indels   4;  Gaps   4;


Qy      53 TGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGG 112
           | |  | ||   | |||||||||||||| | |||||||||||||||||||||||||||||
Db       1 TTCAAGACGAGGCTGAGCTGGCCCCCGCTCACTTCACGCTGCCCCTCCGGGTGGCCGCGG 60


Qy     113 CCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGG-ACCCCTGCCGAGCGCCACGCC 171
           |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db      61 CCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGTGCCCCTGCCGAGCGCCACGCC 120


Qy     172 GACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTC 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTC 180


Qy     232 TTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTG 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTG 240
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Qy    292 ATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCC 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCC 300

Qy    352 GTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA 360

Qy    412 TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTC 471
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Db    361 TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTC 420

Qy    472 GTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATT 531
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Db    421 GTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATT 480

Qy    532 GCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTT 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTT 540

Qy    592 GGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC 600

Qy    652 CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTG 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTG 660

Qy    712 CCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGT 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGT 720

Qy    772 TTGTATAAAGGAGACATCTGGTATA-CCCCTATTAAGGAAGAGTGGTACTACCAGATAGA 830
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    721 TTGTATAAAGGAGACATCTGGTATACCCCCTATTAAGGAAGAGTGGTACTACCAGATAGA 780

Qy    831 AATTCTGAAATTGGAAATT-GGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA-C 888
          |||||||| |||||||||| |||| |||||||||||||||||||||||||||||||| |
Db    781 AATTCTGGAATTGGAAATTGGGAGCCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACC 840

Qy    889 GCAGACAAGGCCATCGTGGACAGTGGCACCACGC 922
          ||||||||| |    |||||||||||||||||||
Db    841 GCAGACAAGCCATCCGTGGACAGTGGCACCACGC 874


RESULT 12
CA454208
LOCUS       CA454208                890 bp    mRNA      linear    EST 12-NOV-2002
DEFINITION  AGENCOURT_10738679 MAPcL Homo sapiens cDNA clone IMAGE:6718872 5',
            mRNA sequence.
ACCESSION   CA454208
VERSION     CA454208.1  GI:24903721
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 890)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
    TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Kristi A. Egland, Ira Pastan
              cDNA Library Preparation: Invitrogen Corp
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM14275 row: n column: 24
             High quality sequence stop: 651.
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                     /clone="IMAGE:6718872"
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                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match   43.9%; Score 792.4; DB 14; Length 890;
  Best Local Similarity   97.9%; Pred. No. 5.1e-107;
    Matches 856; Conservative   0; Mismatches   11; Indels   7; Gaps   5;

Qy   704 CCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTG 763
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTG 60

Qy   764 AACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACC 823
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACC 120

Qy   824 AGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGT 883
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGT 180

Qy   884 ATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGG 943
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGG 240

Qy   944 TGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATG 1003

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                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATG 300

Qy     1004 GTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACT 1063
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACT 360

Qy     1064 TCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAA 1123
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAA 420

Qy     1124 TCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACC 1183
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACC 480

Qy     1184 GATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCT 1243
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCT 540

Qy     1244 TCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAG 1303
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAG 600

Qy     1304 AAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCA 1363
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCA 660

Qy     1364 GCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCA-TTTTGTGGATTGTGTCCTATGCG 1422
                    |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      661 GCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTTGTGGATTGTGTCCTATGCG 720

Qy     1423 CTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTT- 1481
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      721 CTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCCTTC 780

Qy     1482 CCGGTGTCAGCGTCGCCCCC--GTGACCCTGAGGTCGTCAATGATG-AGTCCTCTCTGGT 1538
                    ||||||||||||||||||||    |||||||||||||||||||||| |||||||||||||
Db      781 CCGGTGTCAGCGTCGCCCCCCCGTGACCCCTGAGGTCGTCAATGATGAAGTCCTCTCTGGT 840

Qy     1539 CAGACAT--CGCTGGAAATGAATAGCCAGGCCTG 1570
                    |||||||      | |||| ||||||||||||||
Db      841 CAGACATTCGCTGGAAAATTAATAGCCAGGCCTG 874


RESULT 13
CA488936
LOCUS        CA488936              902 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION   AGENCOURT_10808280 MAPcL Homo sapiens cDNA clone IMAGE:6721142 5',
             mRNA sequence.
ACCESSION    CA488936
VERSION      CA488936.1  GI:24951727
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 902)
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                        /clone="IMAGE:6721142"
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                        hTERT-HME1, LNCaP"
                        /lab_host="EMDH10B"
                        /clone_lib="MAPcL"
                        /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                        Subtracted with brain, liver, lung, kidney and muscle.
                        Directionally cloned. Priming method: oligo-dT. Average
                        insert size: 1800 bp. Library amplification:  26,000 fold.
                        Kristi A. Egland, James J. Vincent, Robert Strausberg,
                        Bungkook Lee & Ira Pastan:  Discovery of new breast
                        cancer genes encoding  membrane and secreted proteins.
                        Manuscript submitted."
ORIGIN
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  Query Match            43.5%;  Score 785.2;  DB 14;  Length 902;
  Best Local Similarity  98.9%;  Pred. No. 5.8e-106;
  Matches  801;  Conservative     0;  Mismatches     8;  Indels    1;  Gaps    1;


Qy      680 TTTTCTCCATGCAGATGTGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TTTTCTCCATGCAGATGTGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 60


Qy      740 GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 120


Qy      800 CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 180


Qy      860 GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 240


Qy      920 CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCAT 979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCAT 300
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Qy     980 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 1039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 360


Qy    1040 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 1099
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Db     361 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACT 420


Qy    1100 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGG 1159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGG 480


Qy    1160 CCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGA 1219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGA 540


Qy    1220 TCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGG 1279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGG 600


Qy    1280 GCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGC 1339
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     601 GCTTCGCAGCGAGCCCCTGTGCAGAAATTGCACGTGCTGCAGTGTCTGAAATTTCCGGGC 660


Qy    1340 CTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCA 1399
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Db     661 CTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCA 720


Qy    1400 -TTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTA 1458
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Db     721 TTTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTA 780


Qy    1459 ATCGTCCTGCTGCTGCTGCCGTTCCGGTGT 1488
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Db     781 ATCGTCCTGCTGCTGCTGGCCGTTCCGGGT 810
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RESULT 14
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LOCUS   CA487940   836 bp   mRNA   linear   EST 14-NOV-2002
DEFINITION AGENCOURT_10810992 MAPcL Homo sapiens cDNA clone IMAGE:6719667 5',
            mRNA sequence.
ACCESSION   CA487940
VERSION   CA487940.1 GI:24948478
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan

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                    cDNA Library Preparation: Invitrogen Corp
                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                    DNA Sequencing by: Agencourt Bioscience Corporation
                    Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM14277  row: p  column: 03
                  High quality sequence stop: 629.
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                          Directionally cloned. Priming method: oligo-dT. Average
                          insert size: 1800 bp. Library amplification: 26,000 fold.
                          Kristi A. Egland, James J. Vincent, Robert Strausberg,
                          Bungkook Lee & Ira Pastan:  Discovery of new breast
                          cancer genes encoding  membrane and secreted proteins.
                          Manuscript submitted."
ORIGIN
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  Query Match               43.1%;  Score 777.4;  DB 14;  Length 836;
  Best Local Similarity     98.2%;  Pred. No. 8.4e-105;
  Matches  818;  Conservative     0;  Mismatches    11;  Indels    4;  Gaps    3;


Qy       468 CTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA 527
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA 60


Qy       528 CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAAT 587
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAAT 120


Qy       588 ACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGA 647
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGA 180


Qy       648 CTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGG 707
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGG 240


Qy       708 CTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACC 767
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACC 300


Qy       768 AAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGAT 827
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Db       301 AAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGAT 360


Qy       828 AGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA 887
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Db     361 AGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA 420

Qy     888 CGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTT 947
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Db     421 CGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTT 480

Qy     948 TGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTT 1007
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTT 540

Qy    1008 CTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC 1067
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC 600

Qy    1068 TAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 1127
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db     601 TAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 660

Qy    1128 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTA-CCGAT 1186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     661 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCCGAT 720

Qy    1187 TCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCA-CGGTGATGGAGGGCTTC 1245
          |||||||||||||    |||||||||||||||||||||||||| || |||||||||||||
Db     721 TCGGCATTTCCCCCATCACAAATGCGCTGGTGATCGGTGCCACCGTTGATGGAGGGCTTC 780

Qy    1246 TACGTCATCTTCGACAGAGCCCAGAA--GAGGGTGGGCTTCGCAGCGAGCCCC 1296
          |||||||||||||||||||||||| |||     || ||||||||||| ||||||||
Db     781 TACGTCATCTTCGACAGAGCCCCGAAAGAGGGTGGGGCTTCGCAACGAGCCCC 833


RESULT 15
BG281374
LOCUS       BG281374                843 bp     mRNA     linear    EST 21-FEB-2001
DEFINITION  602401870F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544392 5',
            mRNA sequence.
ACCESSION   BG281374
VERSION     BG281374.1  GI:13030299
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1227  row: k  column: 17
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High quality sequence stop: 818.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4544392"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_20"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match   43.1%; Score 777.4; DB 12; Length 843;
  Best Local Similarity 97.7%; Pred. No. 8.3e-105;
  Matches   820; Conservative   0; Mismatches   16; Indels   3; Gaps   3;

Qy   765 ACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCA 824
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Db   6 AACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCA 65

Qy   825 GATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTA 884
                |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   66 GATAGAAATTCTGAAATTGGAAA-TGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTA 124

Qy   885 TAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGT 944
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 TAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGT 184

Qy   945 GTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGG 1004
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 GTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGG 244

Qy   1005 TTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTT 1064
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 TTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTT 304

Qy   1065 CCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAAT 1124
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Db   305 CCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAAT 364

Qy   1125 CCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCG 1184
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Qy   1185 ATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTT 1244
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Db   425 ATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTT 484

Qy   1245 CTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGA 1304

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Db        485 CTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGA 544

Qy       1305 AATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAG 1364
                           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAG 604

Qy       1365 CAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCT 1424
                           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCT 664

Qy       1425 CATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCG 1484
                           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCG 724

Qy       1485 GTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACA 1544
                           ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        725 GTGTCAGCGTCGCCCCCGTGA-CCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACA 783

Qy       1545 TCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAA 1603
                           |||   | |||||||||||||| |||| |||||||||| |||||||||||   |  | ||
Db        784 TCGTGGAAAATGAATAGCCAGG-CTGAACTCAAGCAAACATGAACTCAGTATTAGAAAA 841


Search completed: February 28, 2004, 07:03:45
Job time : 4288 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 02:43:37 ; Search time 6893 Seconds
                                          (without alignments)
                              11343.513 Million cell updates/sec

Title: US-09-668-314C-1
Perfect score: 1804
Sequence: 1 atgggcgcactggcccgggc..........aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
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                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
                15: em_ba:*
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                19: em_mu:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	100.0	1804	6	BD235885	BD235885 Alzheimer
2	1804	100.0	1804	6	AR224092	AR224092 Sequence
3	1804	100.0	1804	6	AR269223	AR269223 Sequence
4	1804	100.0	1804	6	AX105383	AX105383 Sequence
5	1804	100.0	1804	6	AX573821	AX573821 Sequence
6	1804	100.0	1804	9	AF200342	AF200342 Homo sapi
7	1790.6	99.3	2990	9	AF178532	AF178532 Homo sapi
8	1788.2	99.1	1885	9	AF200192	AF200192 Homo sapi
9	1784.4	98.9	1879	6	AX376004	AX376004 Sequence
10	1784.4	98.9	1879	9	AY358927	AY358927 Homo sapi
11	1768.2	98.0	1864	9	BC014453	BC014453 Homo sapi
12	1768.2	98.0	1873	6	BD231786	BD231786 Metastati
13	1768.2	98.0	1873	6	AR411231	AR411231 Sequence
14	1768.2	98.0	1873	9	AF117892	AF117892 Homo sapi
15	1765.6	97.9	1862	6	AR136909	AR136909 Sequence
16	1765.6	97.9	1862	6	E30679	E30679 ASP1. 6/200
17	1765.6	97.9	1862	6	AX775211	AX775211 Sequence
18	1765.6	97.9	1862	6	BD165905	BD165905 ASP1. 1/2
19	1765.6	97.9	1862	9	AF204944	AF204944 Homo sapi
20	1753.4	97.2	1863	6	AX351516	AX351516 Sequence
21	1753.4	97.2	1863	9	AF050171	AF050171 Homo sapi
22	1550	85.9	1621	9	AF212252	AF212252 Homo sapi
23	1483.6	82.2	1712	6	AX136403	AX136403 Sequence
24	1483.6	82.2	1712	6	BD123654	BD123654 Secretory
25	1483.6	82.2	1712	9	AK075539	AK075539 Homo sapi
26	1482.2	82.2	2840	9	AF188276	AF188276 Homo sapi
27	1478.6	82.0	2429	6	BD231769	BD231769 Metastati
28	1478.6	82.0	2429	6	AR411214	AR411214 Sequence
29	1442.6	80.0	2821	9	AF188277	AF188277 Homo sapi
30	1263.2	70.0	1494	6	AX879009	AX879009 Sequence
31	1263.2	70.0	1494	6	BD157592	BD157592 Primer fo
32	1263.2	70.0	1494	9	AK027376	AK027376 Homo sapi
33	1179.4	65.4	1774	10	AF216310	AF216310 Mus muscu

	34	1134.2	62.9	1545	6	AR170159	AR170159 Sequence
	35	1134.2	62.9	1545	6	AR201145	AR201145 Sequence
	36	1104.6	61.2	2514	6	AR263854	AR263854 Sequence
	37	953.6	52.9	1021	6	AR263907	AR263907 Sequence
	38	634.6	35.2	3516	5	BC059963	BC059963 Xenopus l
	39	625.2	34.7	2568	5	BC055989	BC055989 Xenopus l
	40	619.6	34.3	972	10	AF051150	AF051150 Mus muscu
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	42	568.6	31.5	845	6	BD146754	BD146754 Primer fo
c	43	496	27.5	554	6	AX136731	AX136731 Sequence
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	45	494	27.4	45566	9	HS44C5	AL773570 Homo sapi

ALIGNMENTS

RESULT 1
BD235885
LOCUS   BD235885   1804 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Alzheimer's disease secretase.
ACCESSION   BD235885
VERSION   BD235885.1 GI:33045655
KEYWORDS   JP 2002526081-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1804)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
             Yan,R.
  TITLE   Alzheimer's disease secretase
  JOURNAL   Patent: JP 2002526081-A 1 20-AUG-2002;
             PHARMACIA AND UPJOHN CO
COMMENT   OS   Homo sapiens (human)
             PN   JP 2002526081-A/1
             PD   20-AUG-2002
             PF   23-SEP-1999 JP 2000574268
             PR   24-SEP-1998 US   60/101594
             PI   MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY PI
             HEINRIKSON,
             PI   LUIS A PARODI,RIQIANG YAN
             PC   C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC
               C12N1/19,
             PC
             C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC
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             Alzheimer's disease secretase
             FH   Key   Location/Qualifiers
             FT   source   1. .1804
             FT   /organism='Homo sapiens (human)'.
FEATURES   Location/Qualifiers
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ORIGIN

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Query Match              100.0%;  Score 1804;  DB 6;  Length 1804;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Db    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Db    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy   1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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Db   1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080

Qy   1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
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Qy   1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
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Qy   1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
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Qy   1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320

Qy   1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
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Qy   1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
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Qy   1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500
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Qy   1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560
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Qy   1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC  1620
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Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy      1801 AAAA 1804
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Db      1801 AAAA 1804
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RESULT 2
AR224092
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LOCUS       AR224092                1804 bp    DNA      linear   PAT 26-SEP-2002
DEFINITION  Sequence 1 from patent US 6440698.
ACCESSION   AR224092
VERSION     AR224092.1  GI:23332752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1804)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 1 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .1804
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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     Query Match            100.0%;  Score 1804;  DB 6;  Length 1804;
     Best Local Similarity  100.0%;  Pred. No. 0;
     Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db      181  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy      241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db      241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy      301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy      361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy      421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy      481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db      481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy      541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db      541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy      601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db      601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy      661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy      721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db      721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy      961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy     1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy    1801 AAAA 1804
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Db    1801 AAAA 1804
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RESULT 3
AR269223
LOCUS   AR269223   1804 bp   DNA   linear   PAT 10-APR-2003

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DEFINITION   Sequence 1 from patent US 6500667.
ACCESSION    AR269223
VERSION      AR269223.1  GI:29700191
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 1804)
  AUTHORS    Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
             Yan,R.
  TITLE      Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL    Patent: US 6500667-A 1 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .1804
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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   Query Match              100.0%;  Score 1804;  DB 6;   Length 1804;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60


Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120


Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180


Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240


Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360


Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420


Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480


Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy    541 TTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    541 TTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
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Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy    1801 AAAA 1804
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Db    1801 AAAA 1804
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RESULT 4
AX105383
LOCUS   AX105383   1804 bp   DNA   linear   PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0123533.
ACCESSION   AX105383
VERSION   AX105383.1 GI:13921510
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE   Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: WO 0123533-A 1 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES   Location/Qualifiers
     source   1. .1804
                     /organism="Homo sapiens"
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ORIGIN

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Query Match              100.0%;  Score 1804;  DB 6;  Length 1804;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 1804; Conservative    0;  Mismatches     0;  Indels    0;  Gaps     0;
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Qy       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

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Qy     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Db     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Db     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
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Db     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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Db    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080

Qy    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
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Db    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140

Qy    1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
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Qy    1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
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Qy    1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
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Qy    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
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Db    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440

Qy    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500
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Db    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500

Qy    1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560

Qy    1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC  1620
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Db    1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC  1620

Qy    1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT  1680
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Db     1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy     1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db     1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy     1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Qy     1801 AAAA 1804
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Db     1801 AAAA 1804
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RESULT 5
AX573821
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LOCUS       AX573821                1804 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 1 from Patent EP1249498.
ACCESSION   AX573821
VERSION     AX573821.1  GI:27551476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: EP 1249498-A 1 16-OCT-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
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ORIGIN
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   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

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Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

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Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db     841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy     901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db     901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy     961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy   1801 AAAA 1804
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Db   1801 AAAA 1804
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RESULT 6
AF200342
LOCUS   AF200342   1804 bp   mRNA   linear   PRI 12-DEC-1999

DEFINITION   Homo sapiens chromosome 21 aspartyl protease 1 mRNA, complete cds.
ACCESSION   AF200342
VERSION   AF200342.1 GI:6561811
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1804)
  AUTHORS   Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
              Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,
              Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
              Gurney,M.E.
  TITLE   Membrane-anchored aspartyl protease with Alzheimer's disease
              beta-secretase activity
  JOURNAL   Nature 402 (6761), 533-537 (1999)
  MEDLINE   20057170
   PUBMED   10591213
REFERENCE   2 (bases 1 to 1804)
  AUTHORS   Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301
              Henrietta, Kalamazoo, MI 49007, USA
FEATURES   Location/Qualifiers
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ORIGIN

   Query Match   100.0%; Score 1804; DB 9; Length 1804;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

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Qy    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy   1801 AAAA 1804
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            | | | |
Db          1801 AAAA 1804


RESULT 7
AF178532
LOCUS       AF178532                2990 bp    mRNA    linear   PRI 21-SEP-2000
DEFINITION  Homo sapiens aspartyl protease (BACE2) mRNA, complete cds.
ACCESSION   AF178532
VERSION     AF178532.1  GI:6851265
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2990)
  AUTHORS   Solans,A., Estivill,X. and de La Luna,S.
  TITLE     A new aspartyl protease on 21q22.3, BACE2, is highly similar to
            Alzheimer's amyloid precursor protein beta-secretase
  JOURNAL   Cytogenet. Cell Genet. 89 (3-4), 177-184 (2000)
  MEDLINE   20422477
   PUBMED   10965118
REFERENCE   2  (bases 1 to 2990)
  AUTHORS   Solans,A., Estivill,X. and de la Luna,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Medical and Molecular Genetics Center, IRO,
            Avia. Castelldefels Km 2,7, L'Hospitalet de Llobregat, Barcelona
            08907, Spain
FEATURES             Location/Qualifiers
     source          1. .2990
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                     CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFST
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                     /gene="BACE2"
     polyA_signal    2959. .2964
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                                    /gene="BACE2"
ORIGIN

   Query Match   99.3%;   Score 1790.6;   DB 9;   Length 2990;
   Best Local Similarity   99.8%;   Pred. No. 0;
   Matches 1793;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 523

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 583

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 643

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   644 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 703

Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 763

Qy   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db   764 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 823

Qy   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   824 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 883

Qy   421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   884 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 943

Qy   481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   944 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 1003

Qy   541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 1063

Qy   601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 1123

Qy   661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db   1124 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 1183

Qy   721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db     1184 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 1243

Qy      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db     1244 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 1303

Qy      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db     1304 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 1363

Qy      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db     1364 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1423

Qy      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db     1424 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1483

Qy     1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db     1484 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1543

Qy     1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1544 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1603

Qy     1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db     1604 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1663

Qy     1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db     1664 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1723

Qy     1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db     1724 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCGGGTGCTGCA 1783

Qy     1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db     1784 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1843

Qy     1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db     1844 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1903

Qy     1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db     1904 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1963

Qy     1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db     1964 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 2023

Qy     1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 2203

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
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Db   2204 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 2260
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RESULT 8
AF200192

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LOCUS       AF200192                1885 bp    mRNA    linear   PRI 16-FEB-2000
DEFINITION  Homo sapiens memapsin 1 mRNA, complete cds.
ACCESSION   AF200192
VERSION     AF200192.1  GI:6470290
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1885)
  AUTHORS   Lin,X., Koelsch,G., Wu,S., Downs,D., Dashti,A. and Tang,J.
  TITLE     Human aspartic protease memapsin 2 cleaves the beta-secretase site
            of beta-amyloid precursor protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)
  MEDLINE   20144060
   PUBMED   10677483
REFERENCE   2  (bases 1 to 1885)
  AUTHORS   Lin,X., Koelsch,G. and Tang,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-OCT-1999) Protein Studies Program, Oklahoma Medical
            Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104,
            USA
FEATURES             Location/Qualifiers
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                     precursor protein"
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        ORIGIN

          Query Match              99.1%;  Score 1788.2;  DB 9;  Length 1885;
          Best Local Similarity    99.8%;  Pred. No. 0;
          Matches 1801;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;


        Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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        Db        78 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 137

        Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
                     ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
        Db       138 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGACCGCGGCCACGAAC 197

        Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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        Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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        Db       258 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 317

        Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db       318 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 377

        Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db       378 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 437

        Qy       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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        Db       438 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 497

        Qy       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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        Qy       481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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        Qy       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy     961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db    1758 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1817

Qy    1741 CTCCCTACTTCCAAGAAAAATAATT-AAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1799
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Db    1818 CTCCCTACTTCCAAGAAAAACAATTAAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1877

Qy    1800 AAAAA 1804
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RESULT 9
AX376004
LOCUS       AX376004                1879 bp    DNA        linear    PAT 01-MAR-2002
DEFINITION  Sequence 71 from Patent WO0168848.
ACCESSION   AX376004
VERSION     AX376004.1  GI:19170395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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ORIGIN

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Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db     454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db     514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

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Db     574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

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Db     634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy     901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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AY358927
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VERSION   AY358927.1 GI:37182971
KEYWORDS   FLI_CDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1879)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE   The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2 (bases 1 to 1879)
  AUTHORS   Clark,H.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Qy       541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db       634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy       601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Qy     841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Qy     901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy     961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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ACCESSION   BC014453
VERSION     BC014453.1  GI:15680203
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 1864)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1864)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
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Two-domain structure, probably arising from ancestral
duplication. This family does not include the retroviral
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smaller and appear to be homologous to a single domain of
the eukaryotic asp proteases"
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ORIGIN

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Best Local Similarity    99.8%;  Pred. No. 0;
Matches 1770;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;


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Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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RESULT 12
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DEFINITION   Metastatic breast and colon cancer regulated genes.
ACCESSION   BD231786
VERSION   BD231786.1 GI:33041556
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1873)
  AUTHORS   Xin,H. and Giese,K.
  TITLE   Metastatic breast and colon cancer regulated genes
  JOURNAL   Patent: JP 2002513542-A 18 14-MAY-2002;
             CHIRON CORP
COMMENT   OS   Homo sapiens (human)
             PN   JP 2002513542-A/18
             PD   14-MAY-2002
             PF   24-DEC-1998 JP 2000526659
             PR   31-DEC-1997 US   60/070112
             PI   HONG XIN,KLAUSE GIESE
             PC   C12N15/00,C07K14/47,C07K16/18,C07K19/00,C12N9/64,C12N15/09, PC
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ORIGIN

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Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db    341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db    401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db    461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db    521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db    581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    641 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db    701 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 760

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 880

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       881 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 940

Qy       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db       941 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 1000

Qy       901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy       961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db      1061 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1120

Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db      1121 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1180

Qy      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db      1181 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1240

Qy      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db      1241 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1300

Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db      1361 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1420

Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db      1421 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1480

Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db      1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db      1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1600

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db      1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1780
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Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAA 1773
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Db      1841 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAA 1873
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RESULT 13
AR411231
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LOCUS       AR411231                1873 bp    DNA        linear    PAT 18-DEC-2003
DEFINITION  Sequence 18 from patent US 6635748.
ACCESSION   AR411231
VERSION     AR411231.1  GI:40163285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1873)
  AUTHORS   Xin,H. and Giese,K.
  TITLE     Metastatic breast and colon cancer regulated genes
  JOURNAL   Patent: US 6635748-A 18 21-OCT-2003;
FEATURES             Location/Qualifiers
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ORIGIN
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   Best Local Similarity  99.8%;   Pred. No. 0;
   Matches 1770;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;
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Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       221 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db       401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460
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Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db    581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    641 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 760

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 880

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    881 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 940

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db    941 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 1000

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db   1001 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1060

Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db   1061 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1120

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db   1121 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1180

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db   1181 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1240

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1241 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1300
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Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db    1301 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1360

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db    1421 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1480

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db    1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db    1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1600

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1780

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db    1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAA 1773
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Db    1841 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAAA 1873
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RESULT 14
AF117892

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LOCUS       AF117892                1873 bp    mRNA    linear   PRI 14-JUL-2000
DEFINITION  Homo sapiens aspartic-like protease mRNA, complete cds.
ACCESSION   AF117892
VERSION     AF117892.1  GI:5565865
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1873)
  AUTHORS   Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U.,
            Kingsley,C. and Giese,K.
  TITLE     Identification of a novel aspartic-like protease differentially
            expressed in human breast cancer cell lines
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FEATURES   Location/Qualifiers
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ORIGIN

     Query Match   98.0%; Score 1768.2; DB 9; Length 1873;
     Best Local Similarity   99.8%; Pred. No. 0;
     Matches 1770; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340

Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db   341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

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Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db    401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db    461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db    521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    641 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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DEFINITION  Sequence 1 from patent US 6162630.
ACCESSION   AR136909
VERSION     AR136909.1  GI:14478159
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1862)
  AUTHORS   Powell,D.J., Southan,C., Chapman,C.G. and Evans,J.R.
  TITLE     ASP1
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FEATURES   Location/Qualifiers
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                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

  Query Match   97.9%;   Score 1765.6;   DB 6;   Length 1862;
  Best Local Similarity 99.8%;   Pred. No. 0;
  Matches 1768; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

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Db     91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db    151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 210

Qy    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db    271 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 330

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db    331 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 390

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Qy     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db     991  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db     1051 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

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Job time : 6912 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 02:44:52 ; Search time 702 Seconds
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Searched: 3373863 seqs, 2124099041 residues

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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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ALIGNMENTS

RESULT 1
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ID   AAA15661 standard; cDNA; 1804 BP.
XX
AC   AAA15661;
XX
DT   03-AUG-2000 (first entry)
XX
DE   Human aspartyl protease 1 (Asp1) nucleotide sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW   Alzheimer's disease; beta secretase site; ss.
XX
OS   Homo sapiens.

PT   New enzyme designated human aspartase useful in research into Alzheimer's
PT   Disease is capable of cleaving amyloid protein precursor at the beta
PT   secretase site to produce amyloid beta peptide.
XX
PS   Claim 11; Fig 1; 183pp; English.
XX
CC   This sequence represents the human aspartyl protease nucleotide sequence.
CC   The invention relates to a protease capable of cleaving the beta
CC   secretase site of amyloid precursor protein (APP). The protease contains
CC   a sequence encoding the amino acid sequence DTG and a sequence encoding
CC   DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC   causes an autosomal dominant form of Alzheimer's disease. APP localises
CC   to the cell surface membrane and have a single C-terminal transmembrane
CC   domain. Proteolytic processing of APP produces the amyloid beta protein,
CC   which is possibly very important in Alzheimer's disease. The invention
CC   includes a nucleotide sequence encoding the protease, a vector containing
CC   the nucleotide sequence, and a cell line comprising the vector. Methods
CC   for screening for inhibitors of beta secretase activity are also given in
CC   the invention. The human aspartase protein and nucleotide sequences and
CC   the methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

     Query Match   100.0%;   Score 1804; DB 3;   Length 1804;
     Best Local Similarity   100.0%;   Pred. No. 0;
     Matches 1804; Conservative   0;   Mismatches   0; Indels   0; Gaps   0;

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Db      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy     1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy    1801 AAAA 1804
           ||||
Db    1801 AAAA 1804
```

RESULT 2
AAS11701

CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing an
CC   APP cleavage site recognisable by a mammalian beta-secretase, and further
CC   comprising two lysine residues at the carboxyl terminus of the amino acid
CC   sequence of the mammalian APP or APP fragment. The polypeptides are used
CC   for assaying for modulators of beta-secretase activity; identifying
CC   agents that inhibit the APP processing activity of human Asp2 aspartyl
CC   protease (Hu-Asp2); identifying agents that modulate the activity of Asp2

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     Query Match              100.0%;   Score 1804;   DB 4;   Length 1804;
     Best Local Similarity    100.0%;   Pred. No. 0;
     Matches 1804;  Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540


Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600


Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy       781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy       901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy       961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy      1801 AAAA 1804
             ||||
Db      1801 AAAA 1804
```

RESULT 3
AAD17864
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ID    AAD17864 standard; cDNA; 1804 BP.
XX
AC    AAD17864;
XX
DT    10-DEC-2001  (first entry)
XX
DE    Human aspartyl protease 1 (hu-Asp1) cDNA.
XX
KW    Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW    Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW    amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW    chromosome 21; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             1. .1557
FT                    /*tag= a
FT                    /product= "Human aspartyl protease 1"
FT    sig_peptide     1. .60
FT                    /*tag= b
FT    mat_peptide     61. .1554
FT                    /*tag= c
FT                    /product= "Mature human aspartyl protease 1"
XX
PN    GB2357767-A.
XX
PD    04-JUL-2001.
XX
```

PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Claim 30; Fig 1; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of
CC   hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC   human Asp1 protein. Asp1 gene is localised on chromosome 21
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

      Query Match   100.0%;   Score 1804;   DB 4;   Length 1804;
      Best Local Similarity   100.0%;   Pred. No. 0;
      Matches 1804;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

```
Qy    241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300

Qy    301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360

Qy    361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420

Qy    421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480

Qy    481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540

Qy    541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600

Qy    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660

Qy    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720

Qy    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780

Qy    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy   1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
```

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Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy   1801 AAAA 1804
          ||||
Db   1801 AAAA 1804


RESULT 4
AAD13020
ID   AAD13020 standard; cDNA; 1804 BP.
XX
```

```
AC    AAD13020;
XX
DT    23-OCT-2001  (first entry)
XX
DE    Human aspartyl protease 1 (Hu-Asp1) cDNA.
XX
KW    Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
KW    beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW    neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW    neuroprotective; antisense therapy; gene therapy; chromosome 21; ss.
XX
OS    Homo sapiens.
XX
FH    Key              Location/Qualifiers
FT    CDS              1. .1557
FT                     /*tag=  a
FT                     /product= "Human aspartyl protease 1 (Hu-Asp1)"
FT    sig_peptide      1. .60
FT                     /*tag=  b
FT    mat_peptide      61. .1554
FT                     /*tag=  c
FT                     /product= "Mature human aspartyl protease 1 (Hu-Asp1)"
XX
PN    WO200150829-A2.
XX
PD    19-JUL-2001.
XX
PF    09-MAY-2001; 2001WO-IB000799.
XX
PR    09-MAY-2001; 2001WO-IB000799.
XX
PA    (BIEN/) BIENKOWSKI M J.
PA    (GURN/) GURNEY M E.
PA    (HEIN/) HEINRIKSON R L.
PA    (PARO/) PARODI L A.
PA    (YANR/) YAN R.
XX
PI    Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR    WPI; 2001-483072/52.
DR    P-PSDB; AAE06858.
XX
PT    Novel purified polypeptide comprising fragment of mammalian aspartyl
PT    protease 2, lacking Asp2 transmembrane domain and retaining beta
PT    secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT    activity.
XX
PS    Example 2; Fig 1; 185pp; English.
XX
CC    The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC    precursor protein (APP) isoforms and their corresponding DNA molecules.
CC    Human aspartyl proteases can act as beta-secretase proteases useful for
CC    treating Alzheimer's disease. APP isoforms are useful for identifying
CC    modulators of amyloid-beta peptide production, for use in designing
CC    therapeutics for the treatment and prevention of Alzheimer's disease,
CC    dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC    and neuronal loss. APP isoforms are also used in methods for identifying
```

CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present cDNA sequence encodes human aspartyl protease 1 (Hu-Asp1). Hu
CC -Asp 1 gene is localised on chromosome 21
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

    Query Match   100.0%;   Score 1804;   DB 4;   Length 1804;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy   421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy   481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy   541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy   601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

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                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        601   TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA   660

Qy        661   CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT   720
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        661   CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT   720

Qy        721   GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA   780
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        721   GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA   780

Qy        781   GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA   840
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        781   GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA   840

Qy        841   TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC   900
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        841   TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC   900

Qy        901   ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG   960
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        901   ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG   960

Qy        961   GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC   1020
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        961   GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC   1020

Qy        1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC   1080
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC   1080

Qy        1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC   1140
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC   1140

Qy        1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA   1200
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA   1200

Qy        1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC   1260
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC   1260

Qy        1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA   1320
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA   1320

Qy        1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT   1380
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT   1380

Qy        1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA   1440
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA   1440

Qy        1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC   1500
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy      1801 AAAA 1804
             ||||
Db      1801 AAAA 1804


RESULT 5
AAD06738
ID     AAD06738 standard; cDNA; 1804 BP.
XX
AC     AAD06738;
XX
DT     10-AUG-2001  (first entry)
XX
DE     Human aspartyl protease 1 (Asp 1) cDNA.
XX
KW     Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW     Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
KW     beta-secretase; chromosome 21; ss.
XX
OS     Homo sapiens.
XX
FH     Key             Location/Qualifiers
FT     CDS             1. .1557
FT                     /*tag=  a
FT                     /product= "Human aspartyl protease 1 (Asp 1)"
FT     sig_peptide     1. .60
FT                     /*tag=  b
FT     sig_peptide     64. .186
FT                     /*tag=  c
FT                     /note= "Pre-pro-peptide"
FT     sig_peptide     67. .186
FT                     /*tag=  d
FT                     /note= "Pro-peptide"
FT     mat_peptide     187. .1554
FT                     /*tag=  e
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FT                    /product= "Human mature aspartyl protease 1 (Asp 1)"
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02580.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 2; Fig 1; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease 1
CC   (Asp 1) cDNA. Asp 1 has alpha-secretase protease and beta-secretase
CC   protease activities. Asp 1 gene is located on chromosome 21
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

     Query Match              100.0%;  Score 1804;  DB 4;  Length 1804;
     Best Local Similarity    100.0%;  Pred. No. 0;
     Matches 1804;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241   GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy     301   CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301   CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy     361   ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361   ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy     421   AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421   AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy     481   GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481   GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy     541   TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541   TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy     601   TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601   TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy     661   CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661   CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy     721   GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721   GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy     781   GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781   GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy     841   TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841   TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy     901   ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901   ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy     961   GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961   GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy     1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy     1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy    1801 AAAA 1804
            ||||
Db    1801 AAAA 1804


RESULT 6
AAS11516
ID   AAS11516 standard; cDNA; 1804 BP.
XX
AC   AAS11516;
XX
```

CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp proteins
CC   and vectors expressing them, and a polypeptide (isoform of amyloid
CC   protein precursor (APP)) comprising the amino acid sequence of an APP or
CC   its fragment containing an APP cleavage site recognizable by a mammalian
CC   beta-secretase, and further comprising two lysine residues at the
CC   carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC   fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC   beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease. APP

CC   comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC   associated with increased levels of Abeta processing is useful in assays
CC   relating the Alzheimer's research. The expression vector is useful for
CC   recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC   oligonucleotides are useful as probes or primers. The probes are useful
CC   for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC   Southern blots. The present sequence encodes human Asp1
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

        Query Match   100.0%;   Score 1804;   DB 4;   Length 1804;
        Best Local Similarity   100.0%;   Pred. No. 0;
        Matches 1804; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy   421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy   481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy   541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy   601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

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Qy     661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy     721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy     781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy    1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy    1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy    1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy     1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy     1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy     1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy     1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy     1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy     1801 AAAA 1804
            ||||
Db     1801 AAAA 1804
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RESULT 7
ABL52456
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ID   ABL52456 standard; cDNA; 1804 BP.
XX
AC   ABL52456;
XX
DT   16-JUL-2002   (first entry)
XX
DE   Human Asp-1 nucleotide sequence SEQ ID NO:1.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KW   proteolytic; chromosome 21; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1. .1557
FT                    /*tag=  a
FT                    /product= "Asp-1"
FT                    /note= "aspartyl protease"
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
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CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the non
CC   -coding strand complementary to a defined 1804 nucleotide sequence (see
CC   ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC   proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence encodes hu-Asp1 from the present invention
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

      Query Match   100.0%;   Score 1804; DB 6;   Length 1804;
      Best Local Similarity   100.0%;   Pred. No. 0;
      Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy     1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
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Db   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy   1801 AAAA 1804
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Db   1801 AAAA 1804

RESULT 8
AAZ34056

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ID    AAZ34056 standard; cDNA; 1879 BP.
XX
AC    AAZ34056;
XX
DT    07-DEC-1999  (first entry)
XX
DE    Human PRO852 nucleotide sequence.
XX
KW    Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW    probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW    secreted protein; transmembrane protein; ss.
XX
OS    Homo sapiens.
XX
PN    WO9946281-A2.
XX
PD    16-SEP-1999.
XX
PF    08-MAR-1999;   99WO-US005028.
XX
PR    10-MAR-1998;   98US-0077450P.
PR    11-MAR-1998;   98US-0077632P.
PR    11-MAR-1998;   98US-0077641P.
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PR    12-MAR-1998;   98US-0077791P.
PR    13-MAR-1998;   98US-0078004P.
PR    17-MAR-1998;   98US-00040220.
PR    20-MAR-1998;   98US-0078886P.
PR    20-MAR-1998;   98US-0078910P.
PR    20-MAR-1998;   98US-0078936P.
PR    20-MAR-1998;   98US-0078939P.
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PR    26-MAR-1998;   98US-0079656P.
PR    27-MAR-1998;   98US-0079663P.
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PR    01-APR-1998;   98US-0080333P.
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PR    08-APR-1998;   98US-0081049P.
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PR    09-APR-1998;   98US-0081203P.
PR    09-APR-1998;   98US-0081229P.
PR    15-APR-1998;   98US-0081817P.
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PR     15-APR-1998;    98US-0081955P.
PR     21-APR-1998;    98US-0082568P.
PR     21-APR-1998;    98US-0082569P.
PR     22-APR-1998;    98US-0082700P.
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PR     23-APR-1998;    98US-0082767P.
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PR     13-MAY-1998;    98US-0085339P.
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PR     22-MAY-1998;    98US-0086392P.
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PR     22-MAY-1998;    98US-0086430P.
PR     22-MAY-1998;    98US-0086486P.
PR     28-MAY-1998;    98US-0087098P.
PR     28-MAY-1998;    98US-0087106P.
PR     28-MAY-1998;    98US-0087208P.
PR     30-JUL-1998;    98US-0094651P.
PR     11-SEP-1998;    98US-0100038P.
XX
PA     (GETH ) GENENTECH INC.
XX
PI     Wood WI,  Goddard A,  Gurney A,  Yuan J,  Baker KP,  Chen J;
XX
DR     WPI; 1999-551358/46.
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DR    P-PSDB; AAY41714.
XX
PT    New secreted and transmembrane polypeptides and their polynucleotides,
PT    useful for treating blood coagulation disorders, cancers and cellular
PT    adhesion disorders.
XX
PS    Claim 2; Fig 72; 530pp; English.
XX
CC    The present invention describes secreted and transmembrane polypeptides
CC    and their polynucleotides. The nucleotide sequences are useful as sources
CC    of probes, primers, for chromosome mapping, and for generation of
CC    antisense sequences. They can also be used to create transgenic animals.
CC    The proteins can be used to treat a variety of diseases and disorders,
CC    depending on their function. Diseases that may be treated include blood
CC    coagulation disorders, cancers and cellular adhesion disorders. They may
CC    also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC    AAY41774 represent polynucleotide and polypeptide sequence given in the
CC    exemplification of the present invention
XX
SQ    Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;
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     Query Match              98.9%;   Score 1784.4;   DB 2;   Length 1879;
     Best Local Similarity    99.9%;   Pred. No. 0;
     Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573
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Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy     1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db     1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy     1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
            ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy     1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy     1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db     1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy     1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db     1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy     1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db      1414  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy      1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db      1474  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy      1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy      1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy      1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy      1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy      1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db      1774  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

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RESULT 9
AAC78500
ID   AAC78500 standard; cDNA; 1879 BP.
XX
AC   AAC78500;
XX
DT   08-FEB-2001   (first entry)
XX
DE   Human PRO852 (UNQ418) nucleotide sequence SEQ ID NO:195.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW   expressed sequence tag; detection; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200053756-A2.
XX
PD   14-SEP-2000.
XX
PF   18-FEB-2000; 2000WO-US004341.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   29-MAR-1999;   99US-0126773P.
PR   21-APR-1999;   99US-0130232P.

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PR    28-APR-1999;   99US-0131445P.
PR    14-MAY-1999;   99US-0134287P.
PR    23-JUN-1999;   99US-0141037P.
PR    26-JUL-1999;   99US-0145698P.
PR    29-OCT-1999;   99US-0162506P.
PR    30-NOV-1999;   99WO-US028313.
PR    02-DEC-1999;   99WO-US028551.
PR    02-DEC-1999;   99WO-US028565.
PR    16-DEC-1999;   99WO-US030095.
PR    30-DEC-1999;   99WO-US031243.
PR    30-DEC-1999;   99WO-US031274.
PR    05-JAN-2000;  2000WO-US000219.
PR    06-JAN-2000;  2000WO-US000277.
PR    06-JAN-2000;  2000WO-US000376.
XX
PA    (GETH ) GENENTECH INC.
XX
PI    Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI    Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI    Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI    Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI    Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR    WPI; 2000-611443/58.
DR    P-PSDB; AAB44270.
XX
PT    Novel PRO polypeptides and polynucleotides used in detection methods, to
PT    target bioactive molecules to specific cells, and to modulate cellular
PT    activities.
XX
PS    Claim 2; Fig 72; 636pp; English.
XX
CC    AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC    tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC    The PRO polynucleotides and polypeptides have cytostatic activity. The
CC    polynucleotides and polypeptides can be used for detecting the presence
CC    of PRO polypeptides in samples, for linking bioactive molecules to cells
CC    and for modulating biological activities of cells, using the polypeptides
CC    for specific targeting. The polypeptide targeting can be used to kill the
CC    target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC    provide specific targeting of bioactive molecules to cells. AAC78600 to
CC    AAC78987 represent PCR primers and probes used in the isolation of the
CC    PRO polynucleotide sequences
XX
SQ    Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

      Query Match              98.9%;  Score 1784.4;  DB 3;  Length 1879;
      Best Local Similarity    99.9%;  Pred. No. 0;
      Matches 1785; Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153


Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213
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Qy    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053
```

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Qy      961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy     1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy     1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy     1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy     1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy     1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy     1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy     1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy     1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy     1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy     1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy     1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy     1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy     1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
            ||||||||||||||||||||||||||||||||||||||||||||||
Db     1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 10
AAS45960
ID   AAS45960 standard; cDNA; 1879 BP.
XX
AC   AAS45960;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Human DNA encoding PRO polypeptide sequence #36.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW   PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006520.
XX
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   06-MAR-2000; 2000US-0186968P.
PR   14-MAR-2000; 2000US-0189320P.
PR   14-MAR-2000; 2000US-0189328P.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000US-0190828P.
PR   21-MAR-2000; 2000US-0191007P.
PR   21-MAR-2000; 2000US-0191048P.
PR   21-MAR-2000; 2000US-0191314P.
PR   28-MAR-2000; 2000US-0192655P.
PR   29-MAR-2000; 2000US-0193032P.
PR   29-MAR-2000; 2000US-0193053P.
PR   30-MAR-2000; 2000WO-US008439.
PR   04-APR-2000; 2000US-0194449P.
PR   04-APR-2000; 2000US-0194647P.
PR   11-APR-2000; 2000US-0195975P.
PR   11-APR-2000; 2000US-0196000P.
PR   11-APR-2000; 2000US-0196187P.
PR   11-APR-2000; 2000US-0196690P.
PR   11-APR-2000; 2000US-0196820P.
PR   18-APR-2000; 2000US-0198121P.
PR   18-APR-2000; 2000US-0198585P.
PR   25-APR-2000; 2000US-0199397P.
PR   25-APR-2000; 2000US-0199550P.
PR   25-APR-2000; 2000US-0199654P.
PR   03-MAY-2000; 2000US-0201516P.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.

Query Match   98.9%;   Score 1784.4;   DB 4;   Length 1879;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1785; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

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                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  333

Qy      241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  393

Qy      301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  453

Qy      361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  513

Qy      421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  573

Qy      481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  633

Qy      541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  693

Qy      601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  753

Qy      661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  813

Qy      721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  873

Qy      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  933

Qy      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  993

Qy      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  1053

Qy      961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1113

Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db   1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db   1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
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Db   1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 11
ABX78563
ID   ABX78563 standard; cDNA; 1879 BP.
XX
AC   ABX78563;
XX

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PR    29-APR-1998;    98US-0083495P.
PR    29-APR-1998;    98US-0083496P.
PR    29-APR-1998;    98US-0083499P.
PR    29-APR-1998;    98US-0083559P.
PR    05-MAY-1998;    98US-0084366P.
PR    06-MAY-1998;    98US-0084414P.
PR    07-MAY-1998;    98US-0084639P.
PR    07-MAY-1998;    98US-0084640P.
PR    07-MAY-1998;    98US-0084643P.
PR    15-MAY-1998;    98US-0085579P.
PR    15-MAY-1998;    98US-0085580P.
PR    15-MAY-1998;    98US-0085582P.
PR    15-MAY-1998;    98US-0085700P.
PR    18-MAY-1998;    98US-0086023P.
PR    22-MAY-1998;    98US-0086392P.
PR    22-MAY-1998;    98US-0086486P.
PR    28-MAY-1998;    98US-0087098P.
PR    28-MAY-1998;    98US-0087208P.
PR    02-JUN-1998;    98US-0087609P.
PR    02-JUN-1998;    98US-0087759P.
PR    03-JUN-1998;    98US-0087827P.
PR    04-JUN-1998;    98US-0088025P.
PR    04-JUN-1998;    98US-0088028P.
PR    04-JUN-1998;    98US-0088029P.
PR    04-JUN-1998;    98US-0088033P.
PR    04-JUN-1998;    98US-0088326P.
PR    05-JUN-1998;    98US-0088167P.
PR    05-JUN-1998;    98US-0088202P.
PR    05-JUN-1998;    98US-0088212P.
PR    05-JUN-1998;    98US-0088217P.
PR    09-JUN-1998;    98US-0088655P.
PR    10-JUN-1998;    98US-0088722P.
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KW   chondrocyte proliferation; chondrocyte differentiation; tumour;
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PN   US2003032127-A1.
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KW   extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW   chondrocyte; proliferation; differentiation; cartilage disorder;
KW   bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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KW   liver; drug screening; transgenic animal; genetic analysis;
KW   antiarthritic; vulnerary; gene therapy; gene; ss.
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PD   06-FEB-2003.
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Matches 1785; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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AC   ACC86929;

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KW    extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW    chondrocyte; proliferation; differentiation; cartilage disorder;
KW    bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW    adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW    liver; drug screening; transgenic animal; genetic analysis;
KW    antiarthritic; vulnerary; gene therapy; gene; ss.
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PF    02-JUL-2002; 2002US-00188773.
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Job time : 723 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 03:40:07 ; Search time 156 Seconds
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Searched: 682709 seqs, 277475446 residues

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     9 1134.2   62.9   1545 4   US-09-912-484-1   Sequence 1, Appli
    10 1104.6   61.2   2514 4   US-09-280-116-32   Sequence 32, Appl
    11   953.6   52.9   1021 4   US-09-280-116-85   Sequence 85, Appl

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12    397.4   22.0    2348   4   US-09-724-566A-42        Sequence 42, Appl
13    397.4   22.0    2348   4   US-09-724-566A-44        Sequence 44, Appl
14    397.4   22.0   16080   4   US-09-724-566A-48        Sequence 48, Appl
15    395     21.9    1503   4   US-09-724-566A-1         Sequence 1, Appli
16    395     21.9    2070   4   US-09-548-372D-3         Sequence 3, Appli
17    395     21.9    2070   4   US-09-548-367D-3         Sequence 3, Appli
18    395     21.9    2070   4   US-09-551-853D-3         Sequence 3, Appli
19    395     21.9    3252   4   US-09-604-608-1          Sequence 1, Appli
20    393.4   21.8    2541   4   US-09-009-191-1          Sequence 1, Appli
21    387.2   21.5    2370   4   US-09-009-191-3          Sequence 3, Appli
22    386     21.4    1380   4   US-09-548-372D-23        Sequence 23, Appl
23    386     21.4    1380   4   US-09-548-367D-23        Sequence 23, Appl
24    386     21.4    1380   4   US-09-551-853D-23        Sequence 23, Appl
25    385     21.3    1362   4   US-09-548-372D-29        Sequence 29, Appl
26    385     21.3    1362   4   US-09-548-367D-29        Sequence 29, Appl
27    385     21.3    1362   4   US-09-551-853D-29        Sequence 29, Appl
28    385     21.3    1380   4   US-09-548-372D-31        Sequence 31, Appl
29    385     21.3    1380   4   US-09-548-367D-31        Sequence 31, Appl
30    385     21.3    1380   4   US-09-551-853D-31        Sequence 31, Appl
31    384.6   21.3    1341   4   US-09-548-372D-21        Sequence 21, Appl
32    384.6   21.3    1341   4   US-09-548-367D-21        Sequence 21, Appl
33    384.6   21.3    1341   4   US-09-551-853D-21        Sequence 21, Appl
34    382.4   21.2    1302   4   US-09-548-372D-25        Sequence 25, Appl
35    382.4   21.2    1302   4   US-09-548-367D-25        Sequence 25, Appl
36    382.4   21.2    1302   4   US-09-551-853D-25        Sequence 25, Appl
37    381     21.1    1506   4   US-09-713-158-1          Sequence 1, Appli
38    381     21.1    2043   4   US-09-548-372D-7         Sequence 7, Appli
39    381     21.1    2043   4   US-09-548-367D-7         Sequence 7, Appli
40    381     21.1    2043   4   US-09-551-853D-7         Sequence 7, Appli
41    380.8   21.1    1278   4   US-09-548-372D-27        Sequence 27, Appl
42    380.8   21.1    1278   4   US-09-548-367D-27        Sequence 27, Appl
43    380.8   21.1    1278   4   US-09-551-853D-27        Sequence 27, Appl
44    294     16.3     306   4   US-09-280-116-52         Sequence 52, Appl
45    291.2   16.1    1977   4   US-09-548-372D-5         Sequence 5, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;   APPLICANT: GURNEY ET AL.
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: 29915/6280I
;   CURRENT APPLICATION NUMBER: US/09/548,372D
;   CURRENT FILING DATE: 2000-04-12
;   PRIOR APPLICATION NUMBER: US 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: US 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23

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  Query Match              100.0%;   Score 1804;   DB 4;   Length 1804;
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  Matches 1804;  Conservative     0;  Mismatches     0;  Indels    0;  Gaps    0;


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Db    1801 AAAA 1804


RESULT 2
US-09-548-367D-1
; Sequence 1, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;   APPLICANT: GURNEY ET AL.
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;   TITLE OF INVENTION:  THEREOF
;   FILE REFERENCE: 29915/6280H
;   CURRENT APPLICATION NUMBER: US/09/548,367D
;   CURRENT FILING DATE:  2000-04-12
;   PRIOR APPLICATION NUMBER: US 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: US 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: US 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn version 3.1
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;   LENGTH: 1804
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;   ORGANISM: Homo sapiens
US-09-548-367D-1

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  Best Local Similarity    100.0%;  Pred. No. 0;
  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy      1801 AAAA 1804
             ||||
Db      1801 AAAA 1804
```

RESULT 3
US-09-551-853D-1
; Sequence 1, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;   APPLICANT: GURNEY ET AL.
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: 29915/6280L
;   CURRENT APPLICATION NUMBER: US/09/551,853D
;   CURRENT FILING DATE: 2000-04-18
;   PRIOR APPLICATION NUMBER: US 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: US 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: US 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-551-853D-1

  Query Match   100.0%; Score 1804; DB 4; Length 1804;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db    181  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  240

Qy    241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300

Qy    301  CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360

Qy    361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420

Qy    421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480

Qy    481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540

Qy    541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600

Qy    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660

Qy    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720

Qy    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780

Qy    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy   1801 AAAA 1804
          ||||
Db   1801 AAAA 1804
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RESULT 4
US-09-215-450-18
; Sequence 18, Application US/09215450

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 Query Match              98.0%;  Score 1768.2;  DB 4;  Length 1873;
 Best Local Similarity    99.8%;  Pred. No. 0;
 Matches 1770;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640


Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      641     TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  700

Qy      601     TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      701     TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  760

Qy      661     CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      761     CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  820

Qy      721     GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      821     GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  880

Qy      781     GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      881     GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  940

Qy      841     TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      941     TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  1000

Qy      901     ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1001    ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  1060

Qy      961     GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1061    GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1120

Qy      1021    CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1121    CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1180

Qy      1081    TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1181    TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1240

Qy      1141    ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1241    ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1300

Qy      1201    TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1301    TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1360

Qy      1261    AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1361    AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1420

Qy      1321    GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1421    GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1480

Qy      1381    CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     · 1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1600

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1601 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1780

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAA 1773
             |||||||||||||||||||||| ||   ||||||||
Db      1841 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAA 1873


RESULT 5
US-08-999-723-1
; Sequence 1, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
;  APPLICANT: Powell, David J.
;  APPLICANT: Southan, Christopher
;  APPLICANT: Chapman, Conrad G.
;  APPLICANT: Evans, Joanne R.
;  TITLE OF INVENTION: ASP1
;  FILE REFERENCE: GH70262
;  CURRENT APPLICATION NUMBER: US/08/999,723A
;  CURRENT FILING DATE: 1997-10-06
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1862
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-999-723-1

  Query Match              97.9%;  Score 1765.6;  DB 3;  Length 1862;
  Best Local Similarity    99.8%;  Pred. No. 0;
  Matches 1768;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       151  GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC  210

Qy       121  CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG  180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       211  CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG  270

Qy       181  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  240
                 |||||||||,||||||||||||||||||||||||||||||||||||||||||||||||||
Db       271  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  330

Qy       241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       331  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  390

Qy       301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  450

Qy       361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       451  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  510

Qy       421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  570

Qy       481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       571  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  630

Qy       541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       631  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  690

Qy       601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
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Db       691  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  750

Qy       661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       751  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  810

Qy       721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
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Db       811  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  870

Qy       781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       871  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  930

Qy       841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       931  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  990

Qy       901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Db    991  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

Qy   1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1170

Qy   1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1171  TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1230

Qy   1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1290

Qy   1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1350

Qy   1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy   1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1470

Qy   1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1530

Qy   1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1590

Qy   1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650

Qy   1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy   1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1770

Qy   1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy   1741  CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1772
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Db   1831  CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAA 1862
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RESULT 6
US-09-434-427-1
; Sequence 1, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
;  APPLICANT: POWELL, DAVID J.
;  APPLICANT: SOUTHAN, CHRISTOPHER
;  APPLICANT: CHAPMAN, CONRAD G.
;  APPLICANT: EVANS, JOANNE R.
;  TITLE OF INVENTION: ASP1
;  FILE REFERENCE: GH-70262-D1
;  CURRENT APPLICATION NUMBER: US/09/434,427
;  CURRENT FILING DATE: 1999-11-04
;  EARLIER APPLICATION NUMBER: US 08/999,723
;  EARLIER FILING DATE: 1997-10-06
;  EARLIER APPLICATION NUMBER: UK 9626022.9
;  EARLIER FILING DATE: 1996-12-14
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1862
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-434-427-1

  Query Match              97.9%;  Score 1765.6;  DB 3;  Length 1862;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1768;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 210

Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      211 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 270

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      271 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 330

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      331 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 390

Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      391 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 450

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db      451  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 510

Qy      421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db      511  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

Qy      481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      571  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 630

Qy      541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      631  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 690

Qy      601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db      691  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 750

Qy      661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db      751  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 810

Qy      721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db      811  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 870

Qy      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      871  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 930

Qy      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db      931  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 990

Qy      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      991  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy      961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1051 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1111 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1170

Qy      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
             ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      1171 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1230

Qy      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1231 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1290

Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1291 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1350
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Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db    1351 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1470

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1471 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1530

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db    1531 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1590

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1591 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1651 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1711 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1770

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1772
           |||||||||||||||||||| ||  |||||||
Db    1831 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAA 1862
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RESULT 7
US-09-215-450-1
; Sequence 1, Application US/09215450
; Patent No. 6635748
; GENERAL INFORMATION:
;   APPLICANT: Giese, Klaus
;   APPLICANT: Xin, Hong
;   TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
;   FILE REFERENCE: 1451.100 / 210030.447
;   CURRENT APPLICATION NUMBER: US/09/215,450
;   CURRENT FILING DATE: 1998-12-17
;   NUMBER OF SEQ ID NOS: 27
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 2429
;   TYPE: DNA
;   ORGANISM: human
US-09-215-450-1

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Query Match              82.0%;  Score 1478.6;  DB 4;  Length 2429;
Best Local Similarity    99.4%;  Pred. No. 0;
Matches 1484;  Conservative     0;  Mismatches     9;  Indels     0;  Gaps     0;

Qy      305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC 364
            | ||   |||||||||||||||||||||||||||||||||||||||||||||||   | |||||
Db      213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGCAGGAAACCC 272

Qy      365 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 424
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Db      273 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 332

Qy      425 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 484
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Db      333 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 392

Qy      485 TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTG 544
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      393 TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTG 452

Qy      545 AATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG 604
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      453 AATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG 512

Qy      605 CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG 664
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      513 CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG 572

Qy      665 CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT 724
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      573 CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT 632

Qy      725 CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG 784
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Db      633 CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG 692

Qy      785 ACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG 844
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      693 ACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG 752

Qy      845 AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG 904
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      753 AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG 812

Qy      905 TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAG 964
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Db      813 TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAG 872

Qy      965 CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC 1024
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      873 CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC 932

Qy     1025 TGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC 1084
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Db      933 TGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC 992

Qy     1085 TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC 1144
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Db      993  TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC 1052

Qy     1145  AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCA 1204
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1053  AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCA 1112

Qy     1205  CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG 1264
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1113  CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG 1172

Qy     1265  CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT 1324
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1173  CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT 1232

Qy     1325  CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT 1384
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Db     1233  CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT 1292

Qy     1385  CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA 1444
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Db     1293  CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA 1352

Qy     1445  TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG 1504
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1353  TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG 1412

Qy     1505  ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA 1564
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1413  ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA 1472

Qy     1565  GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA 1624
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1473  GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA 1532

Qy     1625  GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTC 1684
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1533  GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTC 1592

Qy     1685  CCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC 1744
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1593  CCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC 1652

Qy     1745  CTACTTCCAAGAAAAATAATTAAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
                    |||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db     1653  CTACTTCCAAGAAAAATAATTAAAAAAAAAAACTTCATTCTAAACCAAACAGA 1705
```

RESULT 8
US-09-717-432-1
; Sequence 1, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
;   APPLICANT: ZHU, YUAN
;   APPLICANT: LI, XIAOTONG
;   APPLICANT: CHRISTIE, GARY
;   APPLICANT: POWELL, DAVID J.

```
  Query Match              62.9%;  Score 1134.2;  DB 3;  Length 1545;
  Best Local Similarity    83.6%;  Pred. No. 5.5e-260;
  Matches 1302;  Conservative    0;  Mismatches  243;  Indels   12;  Gaps    1;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            |||||||| |||    || || ||  |||| |   ||||||| ||||||||| || | ||
Db        1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            | ||| | ||||||||||||||||||||||||||||||||||||| |||||| |||||||||
Db       61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCAAGTGGCCGGGGCCACGAAC 120


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            | |  || || |     || |||| |||||||| |    || || ||||| || | ||
Db      121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCCGAGTTGCCCCGGGCCGATGGTCTG 180


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            || |||||| ||||||||| |   |||            | |||||||||||||| |||
Db      181 GCCCTCGCACTGGAGCCTGTCAGGGC-----------TACTGCCAACTTCTTGGCTATG 228


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            || ||||||||| ||||||||||||||||||||||||||||| |||||||||||||||||
Db      229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            || |||||||| |||||||||| || ||||||||||||||||||||| || ||||||||
Db      289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
             |||| ||||||||||||||||||| |||||||| ||||||| ||||||| || ||||||
Db      349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 408


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            |||||||||||| ||||| |||||||||||| ||||||||||||| |||||| |||| ||
Db      409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 468


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||| ||||||||||| |||||||||||| || |||||||| |||| |||||||||||||
Db      469 GACCTTGTCACCATCCCAAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 528


Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            || || || ||||||||||||||||||||| ||||||||||||||||| ||||| || |||
Db      529 TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588
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Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
           |||||   |  | |||||||||||||| |||||||||| || || || ||||||||| |
Db    589 TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGATTCCCTGGTGGCC 648

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
           ||||||||  ||  ||   || ||||||||||||||||| || || || ||||| || |||
Db    649 CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT 708

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
           ||  |||||  ||||||||||||||||||| || |||||||  ||||||||||||||||||
Db    709 GGTTCTGGTACCAACGGAGGTAGTCTTGTCCTGGGTGGGATTGAACCAAGTTTGTATAAA 768

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
           |||||  |||||||||||||||  ||||| || || ||||||||| || ||||||| |||||
Db    769 GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG 828

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
           |||||||||||||||||| | ||| ||| |||||||||||||||||||||||||||||||||
Db    829 TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 888

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
           ||  ||||||||||||||||||| || ||||||||||||||||||||||||||| ||||||
Db    889 ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG 948

Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
           |||||||||||| ||   ||||||||||||||| || ||||||||| ||||||||  || ||
Db    949 GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC 1008

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
           |||||||| ||||||||| ||||| ||||| |||  | ||  || |||||||||| || ||| |||
Db   1009 CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC 1068

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           |||||||||||||||||  ||||| || | || |||||| ||||| || || || |||||  |||
Db   1069 TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCCACAGCTCTAC 1128

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           |||||||||||||||||| || ||  | ||||||||||| ||||| || || || ||| |
Db   1129 ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT 1188

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           ||||||||||||||||||||| ||||| || ||||||||| ||||||||||| |||| |||
Db   1189 TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC 1248

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           |||||  |||  ||||||||||| ||||| ||| ||| ||||||||||| ||  ||||| | ||
Db   1249 AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA 1308

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           ||||||||||||||| |||||| || || || || || || |||||||||||||| || ||
Db   1309 GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA 1368

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           ||| || |||  |||||||| |||||||||||||||||||| || ||||| || ||||||
Db   1369 CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA 1428
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Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           |||||  ||||||  ||   |  |||  ||||  |||||||||  |||  |   ||  |   | |    ||||
Db    1429 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC 1488

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
           ||  |||||||||||  ||  ||  |||||||||||  ||  ||||||||||||||||||||||||||
Db    1489 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1545


RESULT 9
US-09-912-484-1
; Sequence 1, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
;  APPLICANT: Christie, Gary
;  APPLICANT:  Li, Xiaotong
;  APPLICANT:  Powell,  David J.
;  APPLICANT:  Zhu, Yuan
;  TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
;  FILE REFERENCE: GP-70663-D1
;  CURRENT APPLICATION NUMBER: US/09/912,484
;  CURRENT FILING DATE:  2001-07-25
;  PRIOR APPLICATION NUMBER: 60/166,974
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: 09/717,432
;  PRIOR FILING DATE: 2000-11-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1545
;   TYPE: DNA
;   ORGANISM: MUS MUSCULUS
US-09-912-484-1

   Query Match          62.9%;  Score 1134.2;  DB 4;  Length 1545;
   Best Local Similarity    83.6%;  Pred. No. 5.5e-260;
   Matches 1302;  Conservative   0;  Mismatches 243;  Indels  12;  Gaps     1;

Qy       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
           ||||||||| |||     || || ||  |||| |     |||||||| ||||||||| ||  | ||
Db       1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
           |  |||  |  |||||||||||||||||||||||||||||||||    |||||||  |||||||||||
Db      61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
           |  |  ||   ||  |     ||  ||||  |||||||||  |     ||  ||  ||||||  ||  ||
Db     121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCCGAGTTGCCCCGGGCCGATGGTCTG 180

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
           || |||||  ||||||||||| |   |||              |  ||||||||||||| |||
Db     181 GCCCTCGCACTGGAGCCTGTCAGGGC-----------TACTGCCAACTTCTTGGCTATG 228

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
           || |||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288
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Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          || ||||||||| ||||||||| || |||||||||||||||||||| || ||||||||
Db    289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          |||| ||||||||||||||||||| ||||||||| ||||||| ||||||| |||||||||| ||||
Db    349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 408

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          |||||||||| ||||| |||||||||||||||| |||||||||| ||||| ||||| ||
Db    409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 468

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          ||||| |||||||||||| |||||||||| | ||||| | ||||| ||||||||||||
Db    469 GACCTTGTCACCATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 528

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          || || || ||||||||||||||||||||| ||||||||||||||||| ||||| || |||
Db    529 TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          ||||| | | ||||||||||||||||| ||||||||||| || || || ||||||||| |
Db    589 TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGATTCCCTGGTGGCC 648

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||||| || || || ||||||||||||||||||| || || || ||||| || |||
Db    649 CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT 708

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          || ||||| |||||||||||||||||||| ||||||||| ||||||| |||||||||||||||||
Db    709 GGTTCTGGTACCAACGGAGGTAGTCTTGTCCTGGGTGGGATTGAACCAAGTTTGTATAAA 768

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          ||||| |||||||||||||| ||||| || || ||||||||| || ||||||||| |||||
Db    769 GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG 828

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
          ||||||||||||||||| | ||| || |||||||||||||||||||||||||||||||||||||||||
Db    829 TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 888

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
          || |||||||||||||||||||||||| |||||||||||||||||||||||||||| ||||||
Db    889 ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG 948

Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
          |||||||||| || |||||||||||||||| || ||||||| |||||||| |||| ||
Db    949 GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC 1008

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
          |||||||| ||||||||| ||||| ||||| || ||| | || |||||||| || || |||
Db   1009 CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC 1068

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
          ||||||||||||||||||| |||| | || ||||| ||||| || || || ||||| |||
Db   1069 TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCCACAGCTCTAC 1128
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Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           ||||||||||||||||| || ||  | |||||||||||| ||||| || || || ||| |
Db    1129 ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT 1188

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           |||||||||||||||||||||||||| ||||| || ||||||||| ||||||||||| |||| |||
Db    1189 TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC 1248

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           ||||| |||| |||||||||||| |||| ||| ||||||||||| ||||| |||| |  ||
Db    1249 AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA 1308

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           ||||||||||||||| ||||| || || || || ||  ||||||||||||||||| || ||
Db    1309 GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA 1368

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           ||| || |||   ||||||||| ||||||||||||||||||||| || ||||| || |||||||
Db    1369 CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA 1428

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           ||||| |||||| ||  | ||| |||| ||||||||| ||| | | || | | | ||||
Db    1429 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC 1488

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
           || |||||||||| || || ||||||||||| || ||||||||||||||||||||||||
Db    1489 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1545


RESULT 10
US-09-280-116-32
; Sequence 32, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 2514
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: aspartyl proteases
US-09-280-116-32

  Query Match             61.2%;  Score 1104.6;  DB 4;  Length 2514;
  Best Local Similarity   92.9%;  Pred. No. 7.1e-253;
  Matches 1428;  Conservative    0;  Mismatches   64;  Indels   45;  Gaps   24;

Qy     305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC 364
           | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGG-AGGAACCC 271
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Qy    365 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 424
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    272 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 331

Qy    425 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 484
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    332 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 391

Qy    485 TCGTCACCATCCCCAAAGGCTTC-AATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 543
          |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db    392 TCGTCACCATCCCCAAAGGCTTCAAATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 451

Qy    544 GAATCAGA-GAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA 602
          ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 GAATCAGAGGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA 511

Qy    603 TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTG---AC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db    512 TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGAACAC 571

Qy    660 ACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC-GGCTTGCCCGTTG 718
          |    ||   |||  ||||||||||||||||||||||||||||||| |||||||||||||
Db    572 AAGCAAAACATCCCCAAACGTTTTCTCCATGCAGATGTGTGGAGCCGGGCTTGCCCGTTG 631

Qy    719 CTGG------ATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT 773
          |      |  ||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db    632 GCTGGGATTCTGGGGAACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT 691

Qy    774 GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT 833
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    692 GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT 751

Qy    834 TCTGAAATT---GGAAATTGGAGGCCAAAGCCTTAAT------CTGGACTGCAGAGAGTA 884
          |||   || |    | ||| | |||||||||||| |||||         | | ||
Db    752 TCTTGAAATTGGGAAATTGGGAGGCCAAAGCTTTAATTCTTGGGACTGCAGGAGGAGTAT 811

Qy    885 TAACGCAGACAAGG--CCATCGTGGACAGT-GGCACCACGCTGCTGCGCCT--GCCCCAG 939
          ||||||||||||||   |         |||||||| ||||||||||||||||    ||||||
Db    812 TAACGCAGACAAGGGCCATCGTTGGACAGTGGGCACCACGCTGCTGCGCCTTGCCCCCAG 871

Qy    940 AAGGTGTTTGATGCGGTGGT-GGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC 998
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    872 AAGGTGTTTGATGCGGTGGTGGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC 931

Qy    999 TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC 1058
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC 991

Qy   1059 TTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTAT 1118
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    992 TTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTAT 1051

Qy   1119 CACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATG 1178
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 CACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATG 1111

Qy   1179 TTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1238
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1112 TTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1171

Qy    1239 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1172 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1231

Qy    1299 TGCAGAAATTGCA-GGTGCTGC-AGTGTCTGAAATTTCCGGGCCTTTCTC-AACAGAGGA 1355
           |||||||||||| |||||||| ||||||||||||||||||||||||||| |||||||||
Db    1232 TGCAGAAATTGCACGGTGCTGCAAGTGTCTGAAATTTCCGGGCCTTTCTCAAACAGAGGA 1291

Qy    1356 TGTAGCCAG-CAACTGTGTCCCCGCTC-AGTCTTTGAGCGA-GCCCATTTTGTGGATTGT 1412
           ||||||||| ||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db    1292 TGTAGCCAGCCAACTGTGTCCCCGCTCAAGTCTTTGAGCGACGCCCATTTTGTGGATTGT 1351

Qy    1413 GTCC----TATGCGCTCATGAGCGTCTGTGG-AGCCATCCTCCTTGTC-TTAATCGTCCT 1466
           ||||        || |          ||||||||||| |||||||||||||||  |||||
Db    1352 GTCCCTATGCCGCTCAATGAAGCGTCTGTGGAAGCCATCCTCCTTGTCGTTAATTCAGTC 1411

Qy    1467 GCTGCTGC----TGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1522
           ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1412 GCTGCTGCTGCTTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1471

Qy    1523 ATGAGTCCTCTCT-GGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1581
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    1472 ATGAGTCCTCTCTGGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1531

Qy    1582 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1532 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1591

Qy    1642 CGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1592 CGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1651

Qy    1702 TCACTGTCTTTTGATTCTTGATTTTCAAGC-TTTCAAATCCTCCCTACTTCCAAGAAAAA 1760
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    1652 TCACTGTCTTTTGATTCTTGATTTTCAAGCTTTTCAAATCCTCCCTACTTCCAAGAAAAA 1711

Qy    1761 TAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
           ||||||||||||||||||||||||||||||| | |
Db    1712 TAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 1748
```

RESULT 11
US-09-280-116-85
; Sequence 85, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85

```
  Query Match              52.9%;  Score 953.6;  DB 4;   Length 1021;
  Best Local Similarity    98.8%;  Pred. No. 3.7e-217;
  Matches  971;  Conservative   0;  Mismatches  10;  Indels   2;  Gaps   1;


Qy      98 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTG 157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      38 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGAGCCCTG 97


Qy     158 CCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGG 217
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      98 CCGAGCGCCACGCCGACGGCTNGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGG 157


Qy     218 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 217


Qy     278 ACCTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 ACCTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 277


Qy     338 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 337


Qy     398 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 397


Qy     458 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 517
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 457


Qy     518 TTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 TTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 517


Qy     578 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 577


Qy     638 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 637


Qy     698 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      638 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 697

Qy      758 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 817
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      698 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 757

Qy      818 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 877
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      758 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 817

Qy      878 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 937
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      818 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 877

Qy      938 AGAAGGTGTTTGATGC--GGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 995
            |||||||||||||||| |   |   | ||||||||||||||||||||||||||||||||||
Db      878 AGAAGGTGTTTGATGCCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 937

Qy      996 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTG 1055
            |||||||||||||||||||||||||||     ||||||||||||||||||||||||||||
Db      938 CTCTGATGGTTTCTGGACTGGGTCCCACTTGGCGTGCTGGACGAATTCGGAAACACCTTG 997

Qy     1056 GTCTTACTTCCCTAAAATCTCCA 1078
            |||||||||||||||||||| ||
Db      998 GTCTTACTTCCCTAAAATCTTCA 1020



RESULT 12
US-09-724-566A-42
; Sequence 42, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
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   Query Match           22.0%;  Score 397.4;  DB 4;  Length 2348;
   Best Local Similarity 55.0%;  Pred. No. 7.1e-85;
   Matches  863; Conservative    0;  Mismatches  676;  Indels   30;  Gaps    3;


Qy         2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
             ||||  |||    ||| |||     |     ||| ||| ||||||  ||  ||    |  | |

Db       238 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297


Qy        62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
               ||     ||||||  || |     |  ||| |   ||  ||  ||| |||||     |  |

Db       298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357


Qy       122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
              |     |   ||  | ·  ||   | ||    ||        ||   |   |   |||

Db       358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 417


Qy       182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC------------------ 224
             |  || |   ||| ||   || |||  || |  | ||   |||

Db       418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477


Qy       225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
              || |||   |||  ||||| ||||||||||| |||   |  || || |  ||||||||||| |||

Db       478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537


Qy       284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
             |||||        |  || | |||||||||||||| |||  |  ||  ||  || || || ||||||||

Db       538 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597


Qy       344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
             |||||||  ||||        |      |||| ||| ||| | | | |       ||||    ||   ||  ||

Db       598 ACTTTGCAGTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657


Qy       404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
             | |||||||||||     |      |   | ||     |||     ||||| || || |   |||

Db       658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717


Qy       464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
              ||     | |||     ||||| || | |||||||| | ||| |||       ||  | | ||

Db       718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777


Qy       524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
             |||||||||  | || |||||||||||| || |||||  |       ||     || ||| | |

Db       778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 837


Qy       584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
             | || || || || || ||||| |||||| |||       |||||| |||        || |||||| | ||||

Db       838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897


Qy       644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
             | ||||| |||||| |   ||  |   || |  | |||||| | |||||| ||||| | |||||| |

Db       898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957
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Qy      704 CCGGCTTGCCCGT---------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
            | ||||| ||| |       || |     |   |   ||||||  ||  |  || | |
Db      958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 1017

Qy      755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
            | || || || |     |||| | |||   |||||||||||| || ||   |   ||||
Db     1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077

Qy      815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
            |||| || ||| |     ||| ||   |||| ||   || ||   || || ||||||
Db     1078 GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137

Qy      875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
            |||  ||||| |||   ||||||  ||| ||||||||||||||||||||||||  || ||   |||
Db     1138 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197

Qy      935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
            || |||| ||||||||| || |  || || | |        || ||    |      | |
Db     1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257

Qy      995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
            ||  |||||||||||||||    ||  ||||||||  ||||||         ||  ||||
Db     1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317

Qy     1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
            ||     |||||     |||||  |||||||| |  | ||||   ||| |   ||| ||||
Db     1318 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377

Qy     1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
            | ||||| ||||| || |||| ||| | ||| || | | || ||  |  | |  |    |
Db     1378 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 1437

Qy     1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
            | || ||||||   || | ||| || |  || | | |        || || || ||
Db     1438 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497

Qy     1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
            | ||||||||||||||||||  |||| ||   | |||| ||   | | |||||| || | |
Db     1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 1557

Qy     1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
            || | ||    |   |   |   | | | |     |||  |  |  || ||||||    ||
Db     1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 1617

Qy     1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
            |||  | |     |   |   | |   | |   ||  ||| |||| || |   |   | ||
Db     1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677

Qy     1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
            | ||||||| | | |   | | |||| | | |   | || | | |  ||  || || ||
Db     1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737

Qy     1472 TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
            | | ||| ||  | || |   | |  |  || | | |||| |   |  ||||||  ||
Db     1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797

Qy     1532 CTCTGGTCA 1540
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          |  |||  |  |
Db        1798 CCCTGCTGA 1806
```

RESULT 13
US-09-724-566A-44
; Sequence 44, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 2348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-566A-44

```
  Query Match            22.0%;  Score 397.4;  DB 4;  Length 2348;
  Best Local Similarity  55.0%;  Pred. No. 7.1e-85;
  Matches  863;  Conservative    0;  Mismatches  676;  Indels  30;  Gaps    3;

Qy        2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
            ||||  |||   ||| |||     |   ||| |||  |||||| ||  ||   |  | |
Db      238 TGGGGGCAGGCGCCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297

Qy       62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
              ||     ||||||| || |    |  ||| |  ||  || || ||| |||||     |  |
Db      298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357

Qy      122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
              |     |   ||  |  ||  | ||   ||   ||        || |   |   |||
Db      358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 417

Qy      182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGC----------------- 224
              | || |  |||  ||  ||  |||| || | | ||  ||  |    |||
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Db   418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477

Qy   225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
         ||  |||   |||   |||||  ||||||||||   |  || || |  |||||||||| |||
Db   478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537

Qy   284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
         |||||     |  || | |||||||||||| |||  |  || || || || || |||||||
Db   538 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597

Qy   344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
         ||||||| ||||   |    |||| ||| ||| ||| |  |    |||| |  || ||  ||
Db   598 ACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657

Qy   404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
         | ||||||||||| |    |  | |  || |  ||  ||| |||||  || || |  |||
Db   658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717

Qy   464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
         ||       | || |||||  || | |||||||| | ||| ||| | ||   || | | ||
Db   718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777

Qy   524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
         |||||||||  | ||   |||||||||| ||| || ||||| |  ||   || ||| | |
Db   778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 837

Qy   584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
         | || || || || || ||| ||||||   |||||| |||  || || |||||| | ||||
Db   838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897

Qy   644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
         | ||||| |||||| |  | | || |  ||| | |||||| || |||  || || || |
Db   898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957

Qy   704 CCGGCTTGCCCGT---------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
         | |||||| ||| |         ||  |    |   |   |||||| ||  |  || | |
Db   958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 1017

Qy   755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
         | || || || |        ||||| | |||   |||||||||| || ||   |   ||||
Db  1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077

Qy   815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
         ||||| ||  || | |   ||| ||    |||| ||  |  || ||    || || ||||||
Db  1078 GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137

Qy   875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
         ||   ||||| |||   |||||| |||   ||||||||||||||||| ||  || |  |||
Db  1138 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197

Qy   935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
         || |||| |||||||||  | | ||  | || | |         || ||   |    |  |
Db  1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257

Qy   995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
         ||  ||||||||||||||| |   |||  ||||||| ||||||||         || ||||
Db  1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317
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Qy   1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
          ||      |||||     |||||  |||||||  |  | ||||    ||| |  ||| ||||
Db   1318 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377

Qy   1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
          | |||||| |||||| || ||||   ||| | | |||  ||  |  | |  | |      |
Db   1378 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 1437

Qy   1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
          | || |||||||   || | ||| |  | ||  | | |      || || || || || ||
Db   1438 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497

Qy   1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
          | |||||||||||||||||| |||||  |||| || |  | || ||  | | |||||| | |
Db   1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 1557

Qy   1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
          || | || |     | |   | | |        ||| |   |  || |||||     ||
Db   1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 1617

Qy   1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
           |||  | |    |   |   | |   | ||     ||| | |  |   |   |   ||
Db   1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677

Qy   1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
          |  |||||| |         | ||||  |    |||  | ||      |  | || || || ||
Db   1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737

Qy   1472 TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
          | |  | |   ||     |  | || | ||  | ||| | |  ||  |  |||||| ||
Db   1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797

Qy   1532 CTCTGGTCA 1540
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Db   1798 CCCTGCTGA 1806
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RESULT 14
US-09-724-566A-48
; Sequence 48, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Basi, Guriqbal
;   APPLICANT: Doane, Minh Tam
;   APPLICANT: Frigon, No. 6627739mand
;   APPLICANT: John, Varghese
;   APPLICANT: Power, Michael
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Tatsuno, Gwen
;   APPLICANT: Tung, Jay
;   APPLICANT: Wang, Shuwen
;   APPLICANT: McConlogue, Lisa
;   TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;   TITLE OF INVENTION: Methods
;   FILE REFERENCE: 228-US-NEWC2

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   Query Match              22.0%;   Score 397.4;   DB 4;   Length 16080;
   Best Local Similarity    55.0%;   Pred. No. 1.5e-84;
   Matches  863;  Conservative     0;  Mismatches  676;   Indels   30;   Gaps     3;


Qy        2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
            |||| |||    ||| |||       |    ||| |||  |||||| || ||    | | |
Db     1607 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 1666


Qy       62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
             ||      ||||||| || |      |  ||| |  || || ||| ||||     |   |
Db     1667 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 1726


Qy      122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
             |      |  || |   ||   | ||   ||    ||      || |   |   |  |||
Db     1727 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 1786


Qy      182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC----------------- 224
             | || |  ||| || ||| || | || || | ||   |  |||
Db     1787 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 1846


Qy      225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
             || |||   |||   ||||| |||||||||| |||   |  || || || |||||||| |||
Db     1847 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGCTACTACGTGG 1906


Qy      284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
            |||||     | || | |||||||||| ||| |  |  || || || || || || |||||||
Db     1907 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 1966


Qy      344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
            ||||||| ||||   |    |||| ||| ||| ||| | |   |  |||   | |   || ||
Db     1967 ACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 2026


Qy      404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
            | |||||||||||    |    | ||   | ||   |||  ||||| || || |   |||
Db     2027 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 2086
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Qy    464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
           ||    | ||   |||||| || | |||||||| | ||| |||    || | | ||
Db   2087 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 2146

Qy    524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
           |||||||||| | ||   |||||||||| || ||||| |   ||   || || ||| | |
Db   2147 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 2206

Qy    584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
           | || || || || || ||||| |||||| |||    || |||||| | ||||
Db   2207 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 2266

Qy    644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
           | |||||| ||||| | || | || | |||||| | ||||||| |||||| | |||||| |
Db   2267 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 2326

Qy    704 CCGGCTTGCCCGT---------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
           | |||||| ||| |         || |   |   |   |||||| || | || |
Db   2327 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 2386

Qy    755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
           | || || || |        |||| | |||   |||||||||| || || |    ||||
Db   2387 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 2446

Qy    815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
           |||| || || |   ||| ||    |||| ||    || ||    || || ||||||
Db   2447 GGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 2506

Qy    875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
           |||  ||||| |||   |||||| |||  |||||||||||||||||||||||   || || |||
Db   2507 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 2566

Qy    935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
           || |||| |||||| ||| || || ||  | || || | |     || ||    | | | |
Db   2567 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 2626

Qy    995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
           || ||||||||||||||||    ||  ||||||| |||||||         || ||||
Db   2627 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 2686

Qy   1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
           ||    ||||| |||||  ||||||||||| | | |||| |||  | ||| ||| ||||
Db   2687 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 2746

Qy   1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
           | |||||| |||||  | || ||||| ||| | | ||| ||   | | | | |      |
Db   2747 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 2806

Qy   1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
           | || |||||||   || | ||| || | || | |    || || || ||
Db   2807 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 2866

Qy   1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
           ||||||||||||||||| |||| || | ||||  || | | ||||| || |
Db   2867 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 2926
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Qy    1292  GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
             || | ||     |    || |          ||| |    |    || ||||| ||
Db    2927  GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 2986

Qy    1352  AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
             |||  | |    |     |    |   |  ||      ||| | |   |    ||
Db    2987  TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 3046

Qy    1412  TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
             |  ||||||    |     | ||||| |    ||| | ||     |   | || || ||
Db    3047  TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 3106

Qy    1472  TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
             | |  | | |   |  | | | | ||  | | ||| | |    ||||||    ||
Db    3107  GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 3166

Qy    1532  CTCTGGTCA 1540
             | ||| | |
Db    3167  CCCTGCTGA 3175
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RESULT 15
US-09-724-566A-1
; Sequence 1, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Basi, Guriqbal
;   APPLICANT: Doane, Minh Tam
;   APPLICANT: Frigon, No. 6627739mand
;   APPLICANT: John, Varghese
;   APPLICANT: Power, Michael
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Tatsuno, Gwen
;   APPLICANT: Tung, Jay
;   APPLICANT: Wang, Shuwen
;   APPLICANT: McConlogue, Lisa
;   TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;   TITLE OF INVENTION: Methods
;   FILE REFERENCE: 228-US-NEWC2
;   CURRENT APPLICATION NUMBER: US/09/724,566A
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: US 09/501,708
;   PRIOR FILING DATE: 2000-02-10
;   PRIOR APPLICATION NUMBER: 60/119,571
;   PRIOR FILING DATE: 1999-02-10
;   PRIOR APPLICATION NUMBER: 60/139,172
;   PRIOR FILING DATE: 1999-06-15
;   NUMBER OF SEQ ID NOS: 104
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1503
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-566A-1

    Query Match   21.9%; Score 395; DB 4; Length 1503;
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Best Local Similarity   55.6%; Pred. No. 2.2e-84;
 Matches 805; Conservative   0; Mismatches 630; Indels 12; Gaps   2;

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Qy     106 GCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGC 165
           |||   | ||| | | ||   |   ||   ||| | |  |||     | ||  | |
Db      55 GCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC 114

Qy     166 CACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCC 225
           | |      | || | |    ||   | | | ||    |||| |   | |
Db     115 CTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC 174

Qy     226 AACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG 285
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Db     175 AGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG 234

Qy     286 ATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC 345
           |||     | || | |||||||||| || ||  | | || || || || || ||||||||
Db     235 ATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAAC 294

Qy     346 TTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCT 405
           ||||| ||||   |    |||| ||| ||| ||| | |    |||| | |  ||  |||
Db     295 TTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCC 354

Qy     406 AGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG 465
           ||||||||||   |    |   |  | ||   |||   ||||| || || |   |||
Db     355 AGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAA 414

Qy     466 GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC 525
           ||     | ||    ||||| || | |||||||| | |||   |||       || | || |
Db     415 GGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCC 474

Qy     526 AACATTGCCACTATTTTTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGA 585
           |||||||| | ||   |||||||||| ||  | || |||||   |    || ||| | ||
Db     475 AACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGC 534

Qy     586 ATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTC 645
           || || || || || |||||    |||||| |||       || ||||||| | |||||
Db     535 ATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTT 594

Qy     646 GACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC 705
           |||||  ||||| | ||  | |  ||  |  | ||||| ||||||  ||||| | |||||| ||
Db     595 GACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCT 654

Qy     706 GGCTTGCCCGT---------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGT 756
           |||| ||| |        ||   |     |    ||||||| ||  | || | ||
Db     655 GGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGA 714

Qy     757 GGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGG 816
           || || || |    |||| | |||   ||||||||||| || ||   |    ||||||
Db     715 GGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGG 774

Qy     817 TACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGC 876
           || ||   || |   ||| ||    |||| ||    || || || || || ||||||||
Db     775 TATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGC 834

Qy     877 AGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCC 936
           |  |||||| |||      ||||||  |||  |||||||||||||||||||   || ||  |||||
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Db     835 AAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCC 894

Qy     937 CAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTC 996
               |||| |||||||| || |  || || |  |         || ||    |      | |||
Db     895 AAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTC 954

Qy     997 TCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGG 1056
               |||||||||||||| ||     ||||||| |||||||         || ||||||
Db     955 CCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGG 1014

Qy    1057 TCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGT 1116
               |||||     ||||| ||||||| |  | ||||    ||| |  ||| |||||
Db    1015 AACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGC 1074

Qy    1117 ATCACAATCCTGCCTCAGCTTTACATTCAGCCCATG---ATGGGGGCCGGCCTGAATTAT 1173
               ||||| |||||| || |||| ||| | | ||| ||        | ||||        | |
Db    1075 ATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGAC 1134

Qy    1174 GAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTG 1233
               || |||||| || | ||| || | || ||| | |         || || || ||    |
Db    1135 GACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATC 1194

Qy    1234 ATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC 1293
               ||||||||||||||||| || || | |||| || | | | |||||| || | |||
Db    1195 ATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGC 1254

Qy    1294 CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAG 1353
                | || |    | | |  | |     ||| |    || |||||   ||    |
Db    1255 GCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCCTTTTGTCACCTTG 1314

Qy    1354 GATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTG 1413
               || | |    |    |    |   |  ||    ||| | |    |  ||  |
Db    1315 GACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATA 1374

Qy    1414 TCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTG 1473
               ||||||    |        | ||||| |   | || | ||     | | || || || ||
Db    1375 GCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 1434

Qy    1474 CTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCT 1533
               |  |   | |   |      |  | ||  |   ||| | |  |||| |  |||||||  |||
Db    1435 CAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCC 1494

Qy    1534 CTGGTCA 1540
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Db    1495 CTGCTGA 1501
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                         GenCore version 5.1.6
                  Copyright (c) 1993 - 2004  Compugen Ltd.



OM nucleic - nucleic search, using sw model

Run on:          February 28, 2004, 05:52:24 ; Search time 637 Seconds
                                             (without alignments)
                                             10216.436 Million cell updates/sec


Title:           US-09-668-314C-1
Perfect score:   1804
Sequence:        1 atgggcgcactggcccgggc.........aaaccaaaaaaaaaaaaaa 1804


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        2353733 seqs, 1803733377 residues


Total number of hits satisfying chosen parameters:      4707466


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                               SUMMARIES
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Result                  Query
   No.   Score  Match Length DB   ID                        Description
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    2      1804    100.0    1804    9     US-09-795-847-1        Sequence 1, Appli
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ALIGNMENTS

RESULT 1
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; Patent No. US20010016324A1
; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.

    Query Match   100.0%; Score 1804; DB 9; Length 1804;
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RESULT 2
US-09-795-847-1
; Sequence 1, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES

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  Query Match                 100.0%;   Score 1804;   DB 9;   Length 1804;
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Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy    1801 AAAA 1804
           ||||
Db    1801 AAAA 1804
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RESULT 3
US-09-794-743-1
; Sequence 1, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493

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   Query Match                 100.0%;  Score 1804;  DB 9;  Length 1804;
   Best Local Similarity       100.0%;  Pred. No. 0;
   Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60


Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120


Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180


Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240


Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300


Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360


Qy       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420


Qy       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480


Qy       481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540


Qy       541 TTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy    1381 CAGTCTTTGAGCGAGCCCATTTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGTCTTTGAGCGAGCCCATTTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy  1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db  1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy  1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy  1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy  1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db  1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy  1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db  1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy  1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db  1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy  1801 AAAA 1804
          ||||
Db  1801 AAAA 1804
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RESULT 4
US-09-794-748-1
; Sequence 1, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24

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Query Match             100.0%;  Score 1804;  DB 9;  Length 1804;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1804;  Conservative    0;  Mismatches     0;  Indels    0;  Gaps    0;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540


Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600


Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660


Qy      661 CAAGCAAACATCCCCAACGTTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db       661    CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720

Qy       721    GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721    GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780

Qy       781    GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781    GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy       841    TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Db       841    TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy       901    ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901    ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy       961    GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
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Db       961    GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy       1021   CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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Db       1021   CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080

Qy       1081   TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081   TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140

Qy       1141   ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141   ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200

Qy       1201   TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201   TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260

Qy       1261   AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261   AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320

Qy       1321   GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321   GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380

Qy       1381   CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381   CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440

Qy       1441   GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441   GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500

Qy       1501   CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy    1801 AAAA 1804
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Db    1801 AAAA 1804
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RESULT 5
US-09-794-925-1
; Sequence 1, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-925-1

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Query Match            100.0%;  Score 1804;  DB 9;  Length 1804;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1804;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db     781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960

Qy     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020

Qy    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080

Qy    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140

Qy    1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200

Qy    1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260

Qy    1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320

Qy    1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380

Qy    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440

Qy    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC  1500

Qy    1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA  1560

Qy    1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC  1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC  1620

Qy    1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT  1680
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Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy      1801 AAAA 1804
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Db      1801 AAAA 1804
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RESULT 6
US-09-681-442-1
; Sequence 1, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-681-442-1

   Query Match   100.0%; Score 1804; DB 9; Length 1804;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy    61  GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC  120
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Db    61  GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC  120

Qy   121  CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG  180

Qy   181  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG  240

Qy   241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC  300

Qy   301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  360

Qy   361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420

Qy   421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480

Qy   481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540

Qy   541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600
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Db   541  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  600

Qy   601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
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Db   601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660

Qy   661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
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Db   661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720

Qy   721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
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Db   721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780

Qy   781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
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Db   781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840

Qy   841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Db   841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900

Qy   901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Db       901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy       961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy      1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy      1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db      1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy      1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy      1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db      1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy      1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy      1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy      1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy      1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy      1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db      1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741  CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy        1801 AAAA 1804
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Db        1801 AAAA 1804


RESULT 7
US-09-869-414-1
; Sequence 1, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;   APPLICANT: Beinkowski et al.
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;   TITLE OF INVENTION:  THEREFOR
;   FILE REFERENCE: 28341/6280M
;   CURRENT APPLICATION NUMBER: US/09/869,414
;   CURRENT FILING DATE:  2001-06-27
;   PRIOR APPLICATION NUMBER: 09/416,901
;   PRIOR FILING DATE: 1999-10-13
;   PRIOR APPLICATION NUMBER: 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-869-414-1

   Query Match               100.0%;  Score 1804;  DB 10;  Length 1804;
   Best Local Similarity     100.0%;  Pred. No. 0;
   Matches 1804;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db           1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy          61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy         121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy         181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db     1141   ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy     1201   TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db     1201   TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy     1261   AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db     1261   AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy     1321   GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db     1321   GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy     1381   CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db     1441   GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

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Qy     1621   AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy     1741   CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
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Db     1741   CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy     1801   AAAA 1804
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Db     1801   AAAA 1804
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RESULT 8
US-09-548-366-1
; Sequence 1, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:

  Query Match   100.0%;   Score 1804;   DB 10;   Length 1804;
  Best Local Similarity   100.0%;   Pred. No. 0;
  Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db   1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db   61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

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Db   121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy   241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy   301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Qy   361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

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Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Qy    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy    1801 AAAA 1804
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RESULT 9
US-09-978-295A-195
; Sequence 195, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi
;   APPLICANT: Baker Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan
;   APPLICANT: Ferrara, Napoleon
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;  PRIOR APPLICATION NUMBER: 60/085338
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085323
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Query Match           98.9%;  Score 1784.4;  DB 9;  Length 1879;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


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RESULT 10
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; Sequence 195, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

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;   APPLICANT:  Tumas, Daniel
;   APPLICANT:  Williams, P. Mickey
;   APPLICANT:  Wood, William I.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION:  Acids Encoding the Same
;   FILE REFERENCE: P2630P1C27
;   CURRENT APPLICATION NUMBER: US/09/978,697
;   CURRENT FILING DATE:   2001-10-16
;   PRIOR APPLICATION NUMBER: 09/918585
;   PRIOR FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-10-17
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;   PRIOR APPLICATION NUMBER: 60/080105
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;  PRIOR APPLICATION NUMBER: 60/082704
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
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; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704

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Query Match              98.9%;  Score 1784.4;  DB 9;  Length 1879;
Best Local Similarity    99.9%;  Pred. No. 0;
Matches 1785;  Conservative   0;  Mismatches    1;  Indels    0;  Gaps    0;


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Qy      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
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Qy      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
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Db      1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1293

Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
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Db      1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1353

Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
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Db      1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1413

Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
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RESULT 11
US-09-978-192A-195
; Sequence 195, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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;   PRIOR FILING DATE: 1998-04-29
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  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db    454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

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Db    514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

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Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db   1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

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Db   1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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; Sequence 195, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/081070
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    Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


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Db        94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153


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Db       154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213


Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db       214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273


Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db       274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333


Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db       334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393


Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db    394  CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA  453

Qy    361  ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC  420
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Qy    421  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  480
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Db    514  AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA  573

Qy    481  GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT  540
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Qy    601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
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Db    694  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  753

Qy    661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
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Db    754  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  813

Qy    721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
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Qy    781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
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Db    874  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  933

Qy    841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
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Qy    901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
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Db    994  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  1053

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Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
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Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
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Db    1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy    1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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; Publication No. US20030004102A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi
;   APPLICANT: Baker Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan
;   APPLICANT: Ferrara, Napoleon
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy     841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy     901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy     961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy    1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy    1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
           |||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy    1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy    1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy    1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy    1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473
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Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy   1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy   1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy   1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy   1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy   1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy   1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 14
US-09-978-608A-195
; Sequence 195, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

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  Query Match              98.9%;  Score 1784.4;  DB 10;  Length 1879;
  Best Local Similarity    99.9%;  Pred. No. 0;
  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633
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Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy    841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy    901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy    961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy   1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy   1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy   1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy   1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy   1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy   1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy   1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy    1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy    1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy    1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy    1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy    1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy    1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 15
US-09-978-585A-195
; Sequence 195, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

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   Query Match              98.9%;  Score 1784.4;  DB 10;  Length 1879;
   Best Local Similarity    99.9%;  Pred. No. 0;
   Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153


Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213


Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273


Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333


Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393


Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453


Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513


Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573


Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633


Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  693

Qy      601  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694  TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA  753

Qy      661  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754  CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT  813

Qy      721  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA  873

Qy      781  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874  GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA  933

Qy      841  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934  TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC  993

Qy      901  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994  ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG  1053

Qy      961  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054  GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC  1113

Qy     1021  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114  CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC  1173

Qy     1081  TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1140
             ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     1174  TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC  1233

Qy     1141  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1234  ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA  1293

Qy     1201  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1294  TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC  1353

Qy     1261  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1354  AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA  1413

Qy     1321  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1414  GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT  1473

Qy     1381  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1474  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy    1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1534  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy    1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1594  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy    1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1654  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy    1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1714  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy    1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1774  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy    1741  CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
            ||||||||||||||||||||||||||||||||||||||||||||||
Db    1834  CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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Search completed: February 28, 2004, 08:48:42
Job time : 645 secs